

# Sequence Listing

<110> Baker, Kevin  
 Botstein, David  
 Eaton, Dan  
 Ferrara, Napoleone  
 Filvaroff, Ellen  
 Gerritsen, Mary  
 Goddard, Audrey  
 Godowski, Paul  
 Grimaldi, Christopher  
 Gurney, Austin  
 Hillan, Kenneth  
 Kljavin, Ivar  
 Napier, Mary  
 Roy, Margaret  
 Tumas, Daniel  
 Wood, William

<120> SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ACIDS ENCODING THE SAME

<130> P2548P1C1

<150> 60/067,411

<151> December 3, 1997

<150> 60/069,334

<151> December 11, 1997

<150> 60/069335

<151> December 11, 1997

<150> 60/069,278

<151> December 11, 1997

<150> 60/069,425

<151> December 12, 1997

<150> 60/069,696

<151> December 16, 1997

<150> 60/069,694

<151> December 16, 1997

<150> 60/069,702

<151> December 16, 1997

<150> 60/069,870

<151> December 17, 1997

<150> 60/069,873

<151> December 17, 1997

<150> 60/068,017

<151> December 18, 1997

<150> 60/070,440





ttcaaaggaa tgaatgcttt acacgttttg gaaatgagtg caaacctct 850  
 tgataataat gggatagagc caggggcatt tgaaggggtg acggtgttcc 900  
 atatcagaat tgcagaagca aaactgacct cagttcctaa aggettacca 950  
 ccaactttat tggagcttca cttagattat aataaaattt caacagtgga 1000  
 acttgaggat tttaaacgat acaaagaact acaaaggctg ggccataggaa 1050  
 acaacaaaat cacagatata gaaaatggga gtcttgctaa cataccacgt 1100  
 gtgagagaaa tacatttgga aaacaataaa ctaaaaaaaaa tcccttcagg 1150  
 attaccagag ttgaaatacc tccagataat ctcccttcat tctaattcaa 1200  
 ttgcaagagt gggagtaaat gacttctgtc caacagtgcc aaagatgaag 1250  
 aaatctttat acagtgcaat aagtttattc aacaaccggg tgaaatactg 1300  
 ggaaatgcaa cctgcaacat ttcgttgtgt tttgagcaga atgagtgttc 1350  
 agcttgggaa ctttggaatg taataattag taattggtaa tgtccattta 1400  
 atataagatt caaaaatccc tacatttgga atacttgaac tctattaata 1450  
 atggtagtat tatatatata agcaaatata tattctcaag tggtaagtcc 1500  
 actgacttat tttatgacaa gaaatttcaa cggaattttg ccaaactatt 1550  
 gatacataag gggttgagag aaacaagcat ctattgcagt ttcctttttg 1600  
 cgtacaaatg atcttacata aatctcatgc ttgaccattc ctttcttcat 1650  
 aacaaaaaag taagatatcc ggtattttaac actttgttat caagcacatt 1700  
 ttaaaaagaa ctgtactgta aatggaatgc ttgacttagc aaaatttgtg 1750  
 ctctttcatt tgctgttaga aaaacagaat taacaaagac agtaatgtga 1800  
 agagtgcatt acactattct tattcttttag taacttgggt agtactgtaa 1850  
 tatttttaat catcttaaag tatgatttga tataatctta ttgaaattac 1900  
 cttatcatgt cttagagccc gtctttatgt ttaaaactaa tttcttaaaa 1950  
 taaagccttc agtaaagtgt cattaccaac ttgataaatg ctactcataa 2000  
 gagctgggtt ggggctatag catatgcttt ttttttttta attattacct 2050  
 gatttaaaaa tctctgtaaa aacgtgtagt gtttcataaa atctgttaact 2100  
 cgcattttta tgatccgcta ttataagctt ttaatagcat gaaaattgtt 2150  
 aggctatata acattgccac ttcaactcta aggaatattt ttgagatata 2200  
 cctttggaag accttgcttg gaagagcctg gacactaaca attctacacc 2250

aaattgtctc ttcaaatacg tatggactgg ataactctga gaaacacatc 2300  
 tagtataact gaataagcag agcatcaaat taaacagaca gaaaccgaaa 2350  
 gctctatata aatgctcaga gttctttatg tattttcttat tggcattcaa 2400  
 catatgtaaa atcagaaaac agggaaattt tcattaataaa tattgggtttg 2450  
 aaat 2454

<210> 2  
 <211> 379  
 <212> PRT  
 <213> Homo Sapien

<400> 2  
 Met Lys Glu Tyr Val Leu Leu Leu Phe Leu Ala Leu Cys Ser Ala  
 1 5 10 15  
 Lys Pro Phe Phe Ser Pro Ser His Ile Ala Leu Lys Asn Met Met  
 20 25 30  
 Leu Lys Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp  
 35 40 45  
 Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu  
 50 55 60  
 Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro  
 65 70 75  
 Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser Asp Leu  
 80 85 90  
 Gly Leu Thr Ser Val Pro Thr Asn Ile Pro Phe Asp Thr Arg Met  
 95 100 105  
 Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu Asn Asp  
 110 115 120  
 Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn Asn Asn  
 125 130 135  
 Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr Lys Lys  
 140 145 150  
 Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu Ile Pro  
 155 160 165  
 Leu Asn Leu Pro Lys Ser Leu Ala Glu Leu Arg Ile His Glu Asn  
 170 175 180  
 Lys Val Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met Asn Ala  
 185 190 195  
 Leu His Val Leu Glu Met Ser Ala Asn Pro Leu Asp Asn Asn Gly  
 200 205 210



<210> 5  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 5  
 ggggtgacggt gttccatata agaattgcag aagcaaaact gacctcagtt 50

<210> 6  
 <211> 3441  
 <212> DNA  
 <213> Homo Sapien

<400> 6  
 cggacgcgtg ggcggacgcg tgggcccgcg gcaccgcccc cggcccggcc 50  
 ctcgcacctc cgcactcgcg cctccctccc tccgcccgtt cccgcgcct 100  
 cctccctccc tctccccag ctgtcccggt cgcgtcatgc cgagcctccc 150  
 ggccccgcgc gccccgctgc tgcctctcgg gctgctgctg ctccggtccc 200  
 ggccggcccc cggcgccggc ccagagcccc ccgtgctgcc catccgttct 250  
 gagaaggagc cgctgcccgt tcggggagcg gcaggctgca ccttcggcgg 300  
 gaaggcttat gccttggaag agacgtggca ccgggacctt gggcagccat 350  
 tcgggggtgat gcgctgcgtg ctgtgcccct gcgaggcgcc tcagtggggt 400  
 cgcctgacca ggggccttgg cagggtcagc tgcaagaaca tcaaaccaga 450  
 gtgcccaccc ccggcctgtg ggcagccgcg ccagctgccg ggacactgct 500  
 gccagacctg cccccaggag cgcagcagtt cggagcggca gccagcggc 550  
 ctgtccttcg agtatccgcg ggacccggag catcgcagtt atagcgaccg 600  
 cggggagcca ggcgctgagg agcgggcccg tggtagcggc cacacggact 650  
 tcgtggcgct gctgacaggg ccgaggtcgc aggcggtggc acgagccga 700  
 gtctcgctgc tgcgtctag cctccgcttc tctatctcct acaggcggct 750  
 ggaccgcctt accaggatcc gcttctcaga ctccaatggc agtgtcctgt 800  
 ttgagcaccg tgcagcccc acccaagatg gcctggtctg tgggggtgtg 850  
 cgggcagtgc ctccggtgtc tctgcggctc cttagggcag aacagctgca 900  
 tgtggcactt gtgacactca ctcacccttc aggggaggtc tgggggcctc 950  
 tcatccggca ccgggccctg gctgcagaga ccttcagtgc catcctgact 1000  
 ctagaaggcc cccacagca gggcgtaggg ggcacacccc tgctcactct 1050

cagtgcacaca gaggactcct tgcatttttt gctgctcttc cgagggtctgc 1100  
 tggaaccacag gagtggggga ctaaccacag ttcccttgag gctccagatt 1150  
 ctacaccaggg ggcagctact gcgagaactt caggccaatg tctcagccca 1200  
 ggaaccagggc tttgctgagg tgetgcccac cctgacagtc caggagatgg 1250  
 actggctggg gctggggggag ctgcagatgg ccctggagtg ggcaggcagg 1300  
 ccagggtctgc gcatcagtgg acacattgct gccaggaaga gctgcgacgt 1350  
 cctgcaaagt gtcccttggt gggctgatgc cctgatccca gtccagacgg 1400  
 gtgctgcggg ctacagccagc ctacagctgc taggaaatgg ctccctgatc 1450  
 tatcaggtgc aagtggtagg gacaagcagt gaggtggtagg ccatgacact 1500  
 ggagaccaag cctcagcggg gggatcagcg cactgtcctg tgccacatgg 1550  
 ctggactcca gccaggagga cacacggcgg tgggtatctg ccctgggctg 1600  
 ggtgcccag gggctcatat gctgctgcag aatgagctct tcctgaacgt 1650  
 gggcaccaag gacttcccag acggagagct tcggggggcac gtggctgccc 1700  
 tgccctactg tgggcatagc gcccgccatg acacgctgcc cgtgccccta 1750  
 gcaggagccc tgggtgctacc ccctgtgaag agccaagcag cagggcacgc 1800  
 ctggctttcc ttggataccc actgtcacct gcactatgaa gtgctgctgg 1850  
 ctgggcttgg tggctcagaa caaggcactg tcaactgccc cctccttggg 1900  
 cctcctggaa cgcaggggccc tcggcggtg ctgaagggat tctatggctc 1950  
 agaggcccag ggtgtggtga aggacctgga gccggaactg ctgcggcacc 2000  
 tggcaaaagg catggcctcc ctgatgatca ccaccaaggg tagccccaga 2050  
 ggggagctcc gagggcaggt gcacatagcc aaccaatgtg aggttggcgg 2100  
 actgcgcctg gagggcgccg gggccgaggg ggtgcgggcg ctgggggctc 2150  
 cggatacagc ctctgctgcg ccgcctgtgg tgccctggtct cccggcccta 2200  
 gcgcccgcga aacctggtgg tcctgggagg ccccgagacc ccaacacatg 2250  
 cttcttcgag gggcagcagc gccccacgg ggctcgctgg gcgcccact 2300  
 acgaccgct ctgctcactc tgcacctgcc agagacgaac ggtgatctgt 2350  
 gaccgggtgg tgtgcccacc gccagctgc ccacaccggg tgcaggctcc 2400  
 cgaccagtgc tgccctgttt gccctgagaa acaagatgtc agagacttgc 2450  
 cagggtgcc aaggagccgg gaccaggag agggctgcta ttttgatgg 2500





Arg Cys Val Leu Cys	Ala Cys Glu Ala	Pro Gln Trp Gly Arg Arg	80	85	90
Thr Arg Gly Pro Gly	Arg Val Ser Cys	Lys Asn Ile Lys Pro Glu	95	100	105
Cys Pro Thr Pro Ala	Cys Gly Gln Pro	Arg Gln Leu Pro Gly His	110	115	120
Cys Cys Gln Thr Cys	Pro Gln Glu Arg	Ser Ser Ser Glu Arg Gln	125	130	135
Pro Ser Gly Leu Ser	Phe Glu Tyr Pro	Arg Asp Pro Glu His Arg	140	145	150
Ser Tyr Ser Asp Arg	Gly Glu Pro Gly	Ala Glu Glu Arg Ala Arg	155	160	165
Gly Asp Gly His Thr	Asp Phe Val Ala	Leu Leu Thr Gly Pro Arg	170	175	180
Ser Gln Ala Val Ala	Arg Ala Arg Val	Ser Leu Leu Arg Ser Ser	185	190	195
Leu Arg Phe Ser Ile	Ser Tyr Arg Arg	Leu Asp Arg Pro Thr Arg	200	205	210
Ile Arg Phe Ser Asp	Ser Asn Gly Ser	Val Leu Phe Glu His Pro	215	220	225
Ala Ala Pro Thr Gln	Asp Gly Leu Val	Cys Gly Val Trp Arg Ala	230	235	240
Val Pro Arg Leu Ser	Leu Arg Leu Leu	Arg Ala Glu Gln Leu His	245	250	255
Val Ala Leu Val Thr	Leu Thr His Pro	Ser Gly Glu Val Trp Gly	260	265	270
Pro Leu Ile Arg His	Arg Ala Leu Ala	Ala Glu Thr Phe Ser Ala	275	280	285
Ile Leu Thr Leu Glu	Gly Pro Pro Gln	Gln Gly Val Gly Gly Ile	290	295	300
Thr Leu Leu Thr Leu	Ser Asp Thr Glu	Asp Ser Leu His Phe Leu	305	310	315
Leu Leu Phe Arg Gly	Leu Leu Glu Pro	Arg Ser Gly Gly Leu Thr	320	325	330
Gln Val Pro Leu Arg	Leu Gln Ile Leu	His Gln Gly Gln Leu Leu	335	340	345
Arg Glu Leu Gln Ala	Asn Val Ser Ala	Gln Glu Pro Gly Phe Ala	350	355	360
Glu Val Leu Pro Asn	Leu Thr Val Gln	Glu Met Asp Trp Leu Val			

365	370	375
Leu Gly Glu Leu Gln Met Ala Leu Glu	Trp Ala Gly Arg Pro Gly	
380	385	390
Leu Arg Ile Ser Gly His Ile Ala Ala	Arg Lys Ser Cys Asp Val	
395	400	405
Leu Gln Ser Val Leu Cys Gly Ala Asp	Ala Leu Ile Pro Val Gln	
410	415	420
Thr Gly Ala Ala Gly Ser Ala Ser Leu	Thr Leu Leu Gly Asn Gly	
425	430	435
Ser Leu Ile Tyr Gln Val Gln Val Val	Gly Thr Ser Ser Glu Val	
440	445	450
Val Ala Met Thr Leu Glu Thr Lys Pro	Gln Arg Arg Asp Gln Arg	
455	460	465
Thr Val Leu Cys His Met Ala Gly Leu	Gln Pro Gly Gly His Thr	
470	475	480
Ala Val Gly Ile Cys Pro Gly Leu Gly	Ala Arg Gly Ala His Met	
485	490	495
Leu Leu Gln Asn Glu Leu Phe Leu Asn	Val Gly Thr Lys Asp Phe	
500	505	510
Pro Asp Gly Glu Leu Arg Gly His Val	Ala Ala Leu Pro Tyr Cys	
515	520	525
Gly His Ser Ala Arg His Asp Thr Leu	Pro Val Pro Leu Ala Gly	
530	535	540
Ala Leu Val Leu Pro Pro Val Lys Ser	Gln Ala Ala Gly His Ala	
545	550	555
Trp Leu Ser Leu Asp Thr His Cys His	Leu His Tyr Glu Val Leu	
560	565	570
Leu Ala Gly Leu Gly Gly Ser Glu Gln	Gly Thr Val Thr Ala His	
575	580	585
Leu Leu Gly Pro Pro Gly Thr Pro Gly	Pro Arg Arg Leu Leu Lys	
590	595	600
Gly Phe Tyr Gly Ser Glu Ala Gln Gly	Val Val Lys Asp Leu Glu	
605	610	615
Pro Glu Leu Leu Arg His Leu Ala Lys	Gly Met Ala Ser Leu Met	
620	625	630
Ile Thr Thr Lys Gly Ser Pro Arg Gly	Glu Leu Arg Gly Gln Val	
635	640	645
His Ile Ala Asn Gln Cys Glu Val Gly	Gly Leu Arg Leu Glu Ala	
650	655	660

Ala	Gly	Ala	Glu	Gly 665	Val	Arg	Ala	Leu	Gly 670	Ala	Pro	Asp	Thr	Ala 675
Ser	Ala	Ala	Pro	Pro 680	Val	Val	Pro	Gly	Leu 685	Pro	Ala	Leu	Ala	Pro 690
Ala	Lys	Pro	Gly	Gly 695	Pro	Gly	Arg	Pro	Arg 700	Asp	Pro	Asn	Thr	Cys 705
Phe	Phe	Glu	Gly	Gln 710	Gln	Arg	Pro	His	Gly 715	Ala	Arg	Trp	Ala	Pro 720
Asn	Tyr	Asp	Pro	Leu 725	Cys	Ser	Leu	Cys	Thr 730	Cys	Gln	Arg	Arg	Thr 735
Val	Ile	Cys	Asp	Pro 740	Val	Val	Cys	Pro	Pro 745	Pro	Ser	Cys	Pro	His 750
Pro	Val	Gln	Ala	Pro 755	Asp	Gln	Cys	Cys	Pro 760	Val	Cys	Pro	Glu	Lys 765
Gln	Asp	Val	Arg	Asp 770	Leu	Pro	Gly	Leu	Pro 775	Arg	Ser	Arg	Asp	Pro 780
Gly	Glu	Gly	Cys	Tyr 785	Phe	Asp	Gly	Asp	Arg 790	Ser	Trp	Arg	Ala	Ala 795
Gly	Thr	Arg	Trp	His 800	Pro	Val	Val	Pro	Pro 805	Phe	Gly	Leu	Ile	Lys 810
Cys	Ala	Val	Cys	Thr 815	Cys	Lys	Gly	Gly	Thr 820	Gly	Glu	Val	His	Cys 825
Glu	Lys	Val	Gln	Cys 830	Pro	Arg	Leu	Ala	Cys 835	Ala	Gln	Pro	Val	Arg 840
Val	Asn	Pro	Thr	Asp 845	Cys	Cys	Lys	Gln	Cys 850	Pro	Val	Gly	Ser	Gly 855
Ala	His	Pro	Gln	Leu 860	Gly	Asp	Pro	Met	Gln 865	Ala	Asp	Gly	Pro	Arg 870
Gly	Cys	Arg	Phe	Ala 875	Gly	Gln	Trp	Phe	Pro 880	Glu	Ser	Gln	Ser	Trp 885
His	Pro	Ser	Val	Pro 890	Pro	Phe	Gly	Glu	Met 895	Ser	Cys	Ile	Thr	Cys 900
Arg	Cys	Gly	Ala	Gly 905	Val	Pro	His	Cys	Glu 910	Arg	Asp	Asp	Cys	Ser 915
Leu	Pro	Leu	Ser	Cys 920	Gly	Ser	Gly	Lys	Glu 925	Ser	Arg	Cys	Cys	Ser 930
Arg	Cys	Thr	Ala	His 935	Arg	Arg	Pro	Pro	Glu 940	Thr	Arg	Thr	Asp	Pro 945
Glu	Leu	Glu	Lys	Glu	Ala	Glu	Gly	Ser						

<210> 8  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide probe  
  
 <400> 8  
 gactagttct agatcgcgag cggccgccct tttttttttt tttt 44  
  
 <210> 9  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 9  
 cggacgcgtg gggcctgcgc acccagct 28  
  
 <210> 10  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 10  
 gccgctcccc gaacgggcag cggctccttc tcagaa 36  
  
 <210> 11  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 11  
 ggcgcacagc acgcagcgca tcaccccgaa tggctc 36  
  
 <210> 12  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 12  
 gtgctgcccc tccgttctga gaagga 26  
  
 <210> 13

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 13  
gcagggtgct caaacaggac ac 22

<210> 14  
<211> 3231  
<212> DNA  
<213> Homo Sapien

<400> 14  
ggcggagcag ccctagccgc caccgtcgct ctgcagctc tcgtcgccac 50  
tgccacogcc gccgcggtca ctgcgtcctg gctccggctc ccgcgccctc 100  
ccggccggcc atgcagcccc gccgcgcccc ggcccccggg gcgcagctgc 150  
tgcccgogct ggccctgctg ctgctgctgc tcggagcggg gccccgaggc 200  
agctccctgg ccaaccgggt gccgcgcg cccttgctctg cggccgggcc 250  
gtgcgcgcg cagccctgcc ggaatggggg tgtgtgcacc tcgcgccctg 300  
agccggaccc gcagcaccgc gccccgcgcg gcgagcctgg ctacagctgc 350  
acctgccccg ccgggatctc cggcgccaac tgccagcttg ttgcagatcc 400  
ttgtgccagc aacccttgct accatggcaa ctgcagcagc agcagcagca 450  
gcagcagcga tggctacctc tgcatttgca atgaaggcta tgaagggtccc 500  
aactgtgaac aggcacttcc cagtctccca gccactggct ggaccgaatc 550  
catggcacc cgcagcttc agcctgttcc tgctactcag gagcctgaca 600  
aaatcctgcc tcgctctcag gcaacgggtga cactgcctac ctggcagccg 650  
aaaacagggc agaaagtgtg agaaatgaaa tgggatcaag tggaggtgat 700  
cccagatatt gcctgtggga atgccagttc taacagctct gcgggtggcc 750  
gcctggtatc ctttgaagtg ccacagaaca cctcagtcaa gattcggcaa 800  
gatgccactg cctcactgat tttgctctgg aaggtcacgg ccacaggatt 850  
ccaacagtgc tccctcatag atggacgaag tgtgaccccc cttcaggctt 900  
cagggggact ggtcctcctg gaggagatgc tcgccttggg gaataatcac 950  
tttattggtt ttgtgaatga ttctgtgact aagtctattg tggctttgcg 1000  
cttaactctg gtggtgaagg tcagcacctg tgtgccgggg gagagtcacg 1050

caaatgactt	ggagtgttca	ggaaaaggaa	aatgcaccac	gaagccgtca	1100
gaggcaactt	tttcctgtac	ctgtgaggag	cagtacgtgg	gtactttctg	1150
tgaagaatac	gatgcttgcc	agaggaaaacc	ttgccaaaaac	aacgcgagct	1200
gtattgatgc	aaatgaaaag	caagatggga	gcaatttcac	ctgtgtttgc	1250
cttcctgggt	atactggaga	gctttgccag	tccaagattg	attactgcat	1300
cctagacca	tgcagaaatg	gagcaacatg	catttccagt	ctcagtggat	1350
tcacctgcc	gtgtccagaa	ggatacttcg	gatctgcttg	tgaagaaaag	1400
gtggaccctt	gcgcctcgtc	tccgtgccag	aacaacggca	cctgctatgt	1450
ggacggggta	cactttacct	gcaactgcag	cccgggcttc	acagggccga	1500
cctgtgcccc	gcttattgac	ttctgtgccc	tcagcccttg	tgctcatggc	1550
acgtgccgca	gcgtgggcac	cagctacaaa	tgccctctgtg	atccaggtta	1600
ccatggcctc	tactgtgagg	aggaatataa	tgagtgcctc	tccgctccat	1650
gcctgaatgc	agccacctgc	agggacctcg	ttaatggcta	tgagtgtgtg	1700
tgcttggcag	aatacaaagg	aacacactgt	gaattgtaca	aggatccctg	1750
cgctaacgtc	agctgtctga	acggagccac	ctgtgacagc	gacggcctga	1800
atggcacgtg	catctgtgca	cccgggttta	cagggtgaaga	gtgcgacatt	1850
gacataaatg	aatgtgacag	taaccctctg	caccatgggtg	ggagctgcct	1900
ggaccagccc	aatggttata	actgccactg	cccgcatggg	tgggtgggag	1950
caaactgtga	gatccacctc	caatggaagt	ccgggcacat	ggcggagagc	2000
ctcaccaaca	tgccacggca	ctccctctac	atcatcattg	gagccctctg	2050
cgtggccttc	atccttatgc	tgatcatcct	gategtgggg	atttgccgca	2100
tcagccgcat	tgaataccag	ggttcttcca	ggccagccta	tgaggagttc	2150
tacaactgcc	gcagcatcga	cagcgagttc	agcaatgcc	ttgcatccat	2200
ccggcatgcc	aggtttggaa	agaaatcccc	gcctgcaatg	tatgatgtga	2250
gccccatcgc	ctatgaagat	tacagtctctg	atgacaaacc	cttggtcaca	2300
ctgattaata	ctaaagattt	gtaatctttt	tttghattat	ttttcaaaaa	2350
gatgagatac	tacactcatt	taaatatctt	taagaaaata	aaaagcttaa	2400
gaaatttaaa	atgctagctg	ctcaagagtt	ttcagtagaa	tatttaagaa	2450
ctaattttct	gcagctttta	gtttggaaaa	aatattttta	aaacaaaatt	2500





110	115	120
Cys Ile Cys Asn Glu Gly Tyr Glu Gly	Pro Asn Cys Glu Gln Ala	
125	130	135
Leu Pro Ser Leu Pro Ala Thr Gly Trp	Thr Glu Ser Met Ala Pro	
140	145	150
Arg Gln Leu Gln Pro Val Pro Ala Thr	Gln Glu Pro Asp Lys Ile	
155	160	165
Leu Pro Arg Ser Gln Ala Thr Val Thr	Leu Pro Thr Trp Gln Pro	
170	175	180
Lys Thr Gly Gln Lys Val Val Glu Met	Lys Trp Asp Gln Val Glu	
185	190	195
Val Ile Pro Asp Ile Ala Cys Gly Asn	Ala Ser Ser Asn Ser Ser	
200	205	210
Ala Gly Gly Arg Leu Val Ser Phe Glu	Val Pro Gln Asn Thr Ser	
215	220	225
Val Lys Ile Arg Gln Asp Ala Thr Ala	Ser Leu Ile Leu Leu Trp	
230	235	240
Lys Val Thr Ala Thr Gly Phe Gln Gln	Cys Ser Leu Ile Asp Gly	
245	250	255
Arg Ser Val Thr Pro Leu Gln Ala Ser	Gly Gly Leu Val Leu Leu	
260	265	270
Glu Glu Met Leu Ala Leu Gly Asn Asn	His Phe Ile Gly Phe Val	
275	280	285
Asn Asp Ser Val Thr Lys Ser Ile Val	Ala Leu Arg Leu Thr Leu	
290	295	300
Val Val Lys Val Ser Thr Cys Val Pro	Gly Glu Ser His Ala Asn	
305	310	315
Asp Leu Glu Cys Ser Gly Lys Gly Lys	Cys Thr Thr Lys Pro Ser	
320	325	330
Glu Ala Thr Phe Ser Cys Thr Cys Glu	Glu Gln Tyr Val Gly Thr	
335	340	345
Phe Cys Glu Glu Tyr Asp Ala Cys Gln	Arg Lys Pro Cys Gln Asn	
350	355	360
Asn Ala Ser Cys Ile Asp Ala Asn Glu	Lys Gln Asp Gly Ser Asn	
365	370	375
Phe Thr Cys Val Cys Leu Pro Gly Tyr	Thr Gly Glu Leu Cys Gln	
380	385	390
Ser Lys Ile Asp Tyr Cys Ile Leu Asp	Pro Cys Arg Asn Gly Ala	
395	400	405

Thr Cys Ile Ser	Ser Leu Ser Gly Phe	Thr Cys Gln Cys Pro Glu
410		420
Gly Tyr Phe Gly	Ser Ala Cys Glu Glu	Lys Val Asp Pro Cys Ala
425		435
Ser Ser Pro Cys	Gln Asn Asn Gly Thr	Cys Tyr Val Asp Gly Val
440		450
His Phe Thr Cys	Asn Cys Ser Pro Gly	Phe Thr Gly Pro Thr Cys
455		465
Ala Gln Leu Ile	Asp Phe Cys Ala Leu	Ser Pro Cys Ala His Gly
470		480
Thr Cys Arg Ser	Val Gly Thr Ser Tyr	Lys Cys Leu Cys Asp Pro
485		495
Gly Tyr His Gly	Leu Tyr Cys Glu Glu	Glu Tyr Asn Glu Cys Leu
500		510
Ser Ala Pro Cys	Leu Asn Ala Ala Thr	Cys Arg Asp Leu Val Asn
515		525
Gly Tyr Glu Cys	Val Cys Leu Ala Glu	Tyr Lys Gly Thr His Cys
530		540
Glu Leu Tyr Lys	Asp Pro Cys Ala Asn	Val Ser Cys Leu Asn Gly
545		555
Ala Thr Cys Asp	Ser Asp Gly Leu Asn	Gly Thr Cys Ile Cys Ala
560		570
Pro Gly Phe Thr	Gly Glu Glu Cys Asp	Ile Asp Ile Asn Glu Cys
575		585
Asp Ser Asn Pro	Cys His His Gly Gly	Ser Cys Leu Asp Gln Pro
590		600
Asn Gly Tyr Asn	Cys His Cys Pro His	Gly Trp Val Gly Ala Asn
605		615
Cys Glu Ile His	Leu Gln Trp Lys Ser	Gly His Met Ala Glu Ser
620		630
Leu Thr Asn Met	Pro Arg His Ser Leu	Tyr Ile Ile Ile Gly Ala
635		645
Leu Cys Val Ala	Phe Ile Leu Met Leu	Ile Ile Leu Ile Val Gly
650		660
Ile Cys Arg Ile	Ser Arg Ile Glu Tyr	Gln Gly Ser Ser Arg Pro
665		675
Ala Tyr Glu Glu	Phe Tyr Asn Cys Arg	Ser Ile Asp Ser Glu Phe
680		690
Ser Asn Ala Ile	Ala Ser Ile Arg His	Ala Arg Phe Gly Lys Lys

695	700	705
Ser Arg Pro Ala Met Tyr Asp Val Ser Pro Ile Ala Tyr Glu Asp		
710	715	720
Tyr Ser Pro Asp Asp Lys Pro Leu Val Thr Leu Ile Lys Thr Lys		
725	730	735

Asp Leu

<210> 16  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 16  
 tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 17  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 17  
 caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 18  
 <211> 508  
 <212> DNA  
 <213> Homo Sapien

<400> 18  
 ctctggaagg tcacggccac aggattccaa cagtgtctccc tcatagatgg 50  
 acgaaagtgt gacccccctt tcaggctttc aggggggactg gtccctcctgg 100  
 aggagatgct cgccttgagg aataatcact ttattgggttt tgtgaatgat 150  
 tctgtgacta agtctattgt ggctttgcgc ttaactctgg tggatgaagg 200  
 cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagggttcag 250  
 gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttccctgtacc 300  
 tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350  
 gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400  
 aagatgggag caatttcacc tgtgtttgcc ttccctgggta tactggagag 450  
 ctttgccaac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500



<223> Synthetic oligonucleotide probe

<400> 22

cagtgtctccc tcatagatgg acgaaagtgt gacccccctt tcaggcgaga 50

gctttgccaa ccgaactga 69

<210> 23

<211> 1520

<212> DNA

<213> Homo Sapien

<400> 23

gctgagtctg ctgctcctgc tgctgtgtgt ccagcctgta acctgtgcct 50

acaccacgcc agggcccccc agagccctca ccacgttggg cggccccaga 100

gcccacacca tgccggggcac ctacgtctcc tcgaccacac tcagtagtcc 150

cagcaccacag ggccctgcaag agcaggcacg ggccctgatg cgggacttcc 200

cgctcgtgga cggccacaac gacctgcccc tggctctaag gcagggtttac 250

cagaaagggc tacaggatgt taacctgcgc aatttcagct acggccagac 300

cagcctggac aggcttagag atggcctcgt gggcgcccag ttctgggtcag 350

cctatgtgcc atgccagacc caggaccggg atgccctgcg cctcacctcg 400

gagcagattg acctcatacg ccgcatgtgt gcctcctatt ctgagctgga 450

gcttgtgacc tcggctaaag ctctgaacga cactcagaaa ttggcctgcc 500

tcacgggtgt agaggggtggc cactcgctgg acaatagcct ctccatctta 550

cgtaccttct acatgctggg agtgcgctac ctgacgtctca cccacacctg 600

caacacaccc tgggcagaga gctccgctaa gggcgctccac tccttctaca 650

acaacatcag cgggctgact gactttggtg agaagggtggg ggcagaaatg 700

aaccgcctgg gcatgatggt agacttatcc catgtctcag atgctgtggc 750

acggcgggcc ctggaagtgt cacaggcacc tgtgatcttc tccactcgg 800

ctgcccgggg tgtgtgcaac agtgctcgga atgttctga tgacatctg 850

cagcttctga agaagaacgg tggcgctgtg atggtgtctt tgtccatggg 900

agtaatacag tgcaacccat cagccaatgt gtccactgtg gcagatcact 950

tcgaccacat caaggctgtc attggatcca agttcatcgg gattgggtgga 1000

gattatgatg gggccggcaa attccctcag gggctggaag acgtgtccac 1050

ataccgggtc ctgatagagg agttgctgag tcgtggctgg agtgaggaag 1100

agcttcaggg tgccttctgt ggaaacctgc tgcgggtctt cagacaagtg 1150

gaaaagggtac aggaagaaaa caaatggcaa agccccttgg aggacaagtt 1200  
 cccggatgag cagctgagca gttcctgcca ctccgacctc tcacgtctgc 1250  
 gtcagagaca gagtctgact tcaggccagg aactcactga gattcccata 1300  
 cactggacag ccaagttacc agccaagtgg tcagtctcag agtcctcccc 1350  
 ccacatggcc ccagtccttg cagttgtggc caccttccca gtccttattc 1400  
 tgtggctctg atgaccagct tagtcctgcc agatgtcact gtagcaagcc 1450  
 acagacaccc cacaaagttc cctgtgtgtg caggcacaaa tatttctga 1500  
 aataaatggt ttggacatag 1520

<210> 24

<211> 433

<212> PRT

<213> Homo Sapien

<400> 24

Met	Pro	Gly	Thr	Tyr	Ala	Pro	Ser	Thr	Thr	Leu	Ser	Ser	Pro	Ser	1	5	10	15
Thr	Gln	Gly	Leu	Gln	Glu	Gln	Ala	Arg	Ala	Leu	Met	Arg	Asp	Phe	20	25	30	
Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Leu	Val	Leu	Arg	Gln	35	40	45	
Val	Tyr	Gln	Lys	Gly	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	Ser	50	55	60	
Tyr	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	Gly	65	70	75	
Ala	Gln	Phe	Trp	Ser	Ala	Tyr	Val	Pro	Cys	Gln	Thr	Gln	Asp	Arg	80	85	90	
Asp	Ala	Leu	Arg	Leu	Thr	Leu	Glu	Gln	Ile	Asp	Leu	Ile	Arg	Arg	95	100	105	
Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	Lys	110	115	120	
Ala	Leu	Asn	Asp	Thr	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	Glu	125	130	135	
Gly	Gly	His	Ser	Leu	Asp	Asn	Ser	Leu	Ser	Ile	Leu	Arg	Thr	Phe	140	145	150	
Tyr	Met	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	His	Thr	Cys	Asn	155	160	165	
Thr	Pro	Trp	Ala	Glu	Ser	Ser	Ala	Lys	Gly	Val	His	Ser	Phe	Tyr	170	175	180	

Asn	Asn	Ile	Ser	Gly	Leu	Thr	Asp	Phe	Gly	Glu	Lys	Val	Val	Ala	
				185					190					195	
Glu	Met	Asn	Arg	Leu	Gly	Met	Met	Val	Asp	Leu	Ser	His	Val	Ser	
				200					205					210	
Asp	Ala	Val	Ala	Arg	Arg	Ala	Leu	Glu	Val	Ser	Gln	Ala	Pro	Val	
				215					220					225	
Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Gly	Val	Cys	Asn	Ser	Ala	Arg	
				230					235					240	
Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Lys	Asn	Gly	Gly	
				245					250					255	
Val	Val	Met	Val	Ser	Leu	Ser	Met	Gly	Val	Ile	Gln	Cys	Asn	Pro	
				260					265					270	
Ser	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Lys	
				275					280					285	
Ala	Val	Ile	Gly	Ser	Lys	Phe	Ile	Gly	Ile	Gly	Gly	Asp	Tyr	Asp	
				290					295					300	
Gly	Ala	Gly	Lys	Phe	Pro	Gln	Gly	Leu	Glu	Asp	Val	Ser	Thr	Tyr	
				305					310					315	
Pro	Val	Leu	Ile	Glu	Glu	Leu	Leu	Ser	Arg	Gly	Trp	Ser	Glu	Glu	
				320					325					330	
Glu	Leu	Gln	Gly	Val	Leu	Arg	Gly	Asn	Leu	Leu	Arg	Val	Phe	Arg	
				335					340					345	
Gln	Val	Glu	Lys	Val	Gln	Glu	Glu	Asn	Lys	Trp	Gln	Ser	Pro	Leu	
				350					355					360	
Glu	Asp	Lys	Phe	Pro	Asp	Glu	Gln	Leu	Ser	Ser	Ser	Cys	His	Ser	
				365					370					375	
Asp	Leu	Ser	Arg	Leu	Arg	Gln	Arg	Gln	Ser	Leu	Thr	Ser	Gly	Gln	
				380					385					390	
Glu	Leu	Thr	Glu	Ile	Pro	Ile	His	Trp	Thr	Ala	Lys	Leu	Pro	Ala	
				395					400					405	
Lys	Trp	Ser	Val	Ser	Glu	Ser	Ser	Pro	His	Met	Ala	Pro	Val	Leu	
				410					415					420	
Ala	Val	Val	Ala	Thr	Phe	Pro	Val	Leu	Ile	Leu	Trp	Leu			
				425					430						

<210> 25

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25  
 agttctggtc agcctatgtg cc 22

<210> 26  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 26  
 cgtgatgggtg tctttgtcca tggg 24

<210> 27  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 27  
 ctccaccaat cccgatgaac ttgg 24

<210> 28  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 28  
 gagcagattg acctcatacg ccgcatgtgt gcctcctatt ctgagctgga 50

<210> 29  
 <211> 1416  
 <212> DNA  
 <213> Homo Sapien

<400> 29  
 aaaacctata aatattccgg attattcata ccgtcccacc atcgggcgcg 50  
 gatccgcggc cggaattct aaaccaacat gccgggcacc tacgctccct 100  
 cgaccacact cagtagtccc agcaccagg gcctgcaaga gcaggcacgg 150  
 gcctgatgc gggacttccc gctcgtggac ggcoacaacg acctgcccct 200  
 ggtcctaagg caggtttacc agaaagggct acaggatggt aacctgcgca 250  
 atttcagcta cggccagacc agcctggaca ggcttagaga tggcctcgtg 300  
 ggcgcccagt tctggtcagc ctatgtgcca tgccagaccc aggaccggga 350  
 tgccctgcgc ctcaccctgg agcagattga cctcatacgc cgcattgtgtg 400



cctcctatct	tgagctggag	cttgtgacct	eggctaaagc	tctgaacgac	450
actcagaaat	tggcctgcct	catcggtgta	gaggggtggcc	actcgctgga	500
caatagcctc	tccatcttac	gtaccttcta	catgctggga	gtgcgctacc	550
tgacgctcac	ccacacctgc	aacacacctt	gggcagagag	ctccgctaag	600
ggcgtccact	ccttctacaa	caacatcagc	gggctgactg	actttggtga	650
gaagggtggtg	gcagaaatga	accgcctggg	catgatggta	gacttatccc	700
atgtctcaga	tgctgtggca	cggcgggccc	tggaaagtgtc	acaggcacct	750
gtgatcttct	cccactcggc	tgccccgggt	gtgtgcaaca	gtgctcggaa	800
tgttcctgat	gacatcctgc	agcttctgaa	gaagaacggt	ggcgtcgtga	850
tggtgtcttt	gtccatggga	gtaatacagt	gcaaccctac	agccaatgtg	900
tccactgtgg	cagatcactt	cgaccacatc	aaggctgtca	ttggatccaa	950
gttcacggg	attggtggag	attatgatgg	ggccggcaaa	ttccctcagg	1000
ggctggaaga	cgtgtccaca	tacccggtcc	tgatagagga	gttgctgagt	1050
cgtggctgga	gtgaggaaga	gcttcagggt	gtccttcgtg	gaaacctgct	1100
gcgggtcttc	agacaagtgg	aaaaggtaca	ggaagaaaac	aaatggcaaa	1150
gccccttgga	ggacaagttc	cgggatgagc	agctgagcag	ttcctgccac	1200
tccgacctct	cacgtctgcg	tcagagacag	agtctgactt	caggccagga	1250
actcactgag	attcccatac	actggacagc	caagttacca	gccaaagtgt	1300
cagtctcaga	gtcctcccc	cacctgaca	aaactcacac	atgccaccg	1350
tgcccagcac	ctgaactcct	ggggggaccg	tcagtcttcc	tcttcccccc	1400
aaaacccaag	gacacc				1416

```
<210> 30
<211> 446
<212> PRT
<213> Homo Sapien
```

```

<400> 30
Met  Pro  Gly  Thr  Tyr  Ala  Pro  Ser  Thr  Thr  Leu  Ser  Ser  Pro  Ser
   1              5              10              15

Thr  Gln  Gly  Leu  Gln  Glu  Gln  Ala  Arg  Ala  Leu  Met  Arg  Asp  Phe
              20              25              30

Pro  Leu  Val  Asp  Gly  His  Asn  Asp  Leu  Pro  Leu  Val  Leu  Arg  Gln
              35              40              45

Val  Tyr  Gln  Lys  Gly  Leu  Gln  Asp  Val  Asn  Leu  Arg  Asn  Phe  Ser

```

				50					55					60
Tyr	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	Gly
				65					70					75
Ala	Gln	Phe	Trp	Ser	Ala	Tyr	Val	Pro	Cys	Gln	Thr	Gln	Asp	Arg
				80					85					90
Asp	Ala	Leu	Arg	Leu	Thr	Leu	Glu	Gln	Ile	Asp	Leu	Ile	Arg	Arg
				95					100					105
Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	Lys
				110					115					120
Ala	Leu	Asn	Asp	Thr	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	Glu
				125					130					135
Gly	Gly	His	Ser	Leu	Asp	Asn	Ser	Leu	Ser	Ile	Leu	Arg	Thr	Phe
				140					145					150
Tyr	Met	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	His	Thr	Cys	Asn
				155					160					165
Thr	Pro	Trp	Ala	Glu	Ser	Ser	Ala	Lys	Gly	Val	His	Ser	Phe	Tyr
				170					175					180
Asn	Asn	Ile	Ser	Gly	Leu	Thr	Asp	Phe	Gly	Glu	Lys	Val	Val	Ala
				185					190					195
Glu	Met	Asn	Arg	Leu	Gly	Met	Met	Val	Asp	Leu	Ser	His	Val	Ser
				200					205					210
Asp	Ala	Val	Ala	Arg	Arg	Ala	Leu	Glu	Val	Ser	Gln	Ala	Pro	Val
				215					220					225
Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Gly	Val	Cys	Asn	Ser	Ala	Arg
				230					235					240
Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Lys	Asn	Gly	Gly
				245					250					255
Val	Val	Met	Val	Ser	Leu	Ser	Met	Gly	Val	Ile	Gln	Cys	Asn	Pro
				260					265					270
Ser	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Lys
				275					280					285
Ala	Val	Ile	Gly	Ser	Lys	Phe	Ile	Gly	Ile	Gly	Gly	Asp	Tyr	Asp
				290					295					300
Gly	Ala	Gly	Lys	Phe	Pro	Gln	Gly	Leu	Glu	Asp	Val	Ser	Thr	Tyr
				305					310					315
Pro	Val	Leu	Ile	Glu	Glu	Leu	Leu	Ser	Arg	Gly	Trp	Ser	Glu	Glu
				320					325					330
Glu	Leu	Gln	Gly	Val	Leu	Arg	Gly	Asn	Leu	Leu	Arg	Val	Phe	Arg
				335					340					345



atatacttggga	tgtggtgacc	acggaccccc	cgccccagct	gcacgtgagc	850
cgcgctcgggg	gcctggagga	ccagctgagc	gtgcgctggg	tgtcgccacc	900
cgccctcaag	gatttcctct	ttcaagccaa	ataccagatc	cgctaccgag	950
tggaggacag	tgtggactgg	aaggtggtgg	acgatgtgag	caaccagacc	1000
tcttgccgcc	tggccggcct	gaaacccggc	accgtgtact	tcgtgcaagt	1050
gcgctgcaac	ccctttggca	tctatggctc	caagaaagcc	gggatctgga	1100
gtgagtggag	ccacccaca	gccgcctcca	ctccccgcag	tgagcgcccg	1150
ggcccgggcg	gcggggcgctg	cgaaccgcgg	ggcggagagc	cgagctcggg	1200
gccggtgcgg	cgcgagctca	agcagttcct	gggctggctc	aagaagcacg	1250
cgtactgctc	caacctcagc	ttccgcctct	acgaccagtg	gcgagcctgg	1300
atgcagaagt	cgcacaaagac	ccgcaaccag	gacgagggga	tcttgccctc	1350
gggcagacgg	ggcacggcga	gaggtcctgc	cagataagct	gtaggggctc	1400
agggccacct	ccctgccacg	tggagacgca	gaggccgaac	ccaaactggg	1450
gccacctctg	tacctctact	tcagggcacc	tgagccaccc	tcagcaggag	1500
ctgggggtggc	ccctgagctc	caacggccat	aacagctctg	actcccacgt	1550
gaggccacct	ttgggtgcac	cccagtgggt	gtgtgtgtgt	gtgtgagggt	1600
tggttgagtt	gcctagaacc	cctgccaggg	ctgggggtga	gaaggggagt	1650
cattactccc	cattacctag	ggccccctcca	aaagagtcct	tttaaataaa	1700
tgagctattt	aggtgctgtg	attgtgaaaa	aaaaaaaaaa	aaaaaaaaaa	1750
aaaaaaaaaa	aaaaaaaaaa	aaaaacaaaa	aaaaaaaaaa	1790	

```
<210> 32
<211> 422
<212> PRT
<213> Homo Sapien
```

```
<400> 32
Met Pro Ala Gly Arg Arg Gly Pro Ala Ala Gln Ser Ala Arg Arg
   1                               5               10              15

Pro Pro Pro Leu Leu Pro Leu Leu Leu Leu Cys Val Leu Gly
      20                25              30

Ala Pro Arg Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
      35                40              45

Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Leu Ala Thr Cys
      50                55              60
```

Ser	Val	His	Gly	Asp 65	Pro	Pro	Gly	Ala	Thr 70	Ala	Glu	Gly	Leu	Tyr 75
Trp	Thr	Leu	Asn	Gly 80	Arg	Arg	Leu	Pro	Pro 85	Glu	Leu	Ser	Arg	Val 90
Leu	Asn	Ala	Ser	Thr 95	Leu	Ala	Leu	Ala	Leu 100	Ala	Asn	Leu	Asn	Gly 105
Ser	Arg	Gln	Arg	Ser 110	Gly	Asp	Asn	Leu	Val 115	Cys	His	Ala	Arg	Asp 120
Gly	Ser	Ile	Leu	Ala 125	Gly	Ser	Cys	Leu	Tyr 130	Val	Gly	Leu	Pro	Pro 135
Glu	Lys	Pro	Val	Asn 140	Ile	Ser	Cys	Trp	Ser 145	Lys	Asn	Met	Lys	Asp 150
Leu	Thr	Cys	Arg	Trp 155	Thr	Pro	Gly	Ala	His 160	Gly	Glu	Thr	Phe	Leu 165
His	Thr	Asn	Tyr	Ser 170	Leu	Lys	Tyr	Lys	Leu 175	Arg	Trp	Tyr	Gly	Gln 180
Asp	Asn	Thr	Cys	Glu 185	Glu	Tyr	His	Thr	Val 190	Gly	Pro	His	Ser	Cys 195
His	Ile	Pro	Lys	Asp 200	Leu	Ala	Leu	Phe	Thr 205	Pro	Tyr	Glu	Ile	Trp 210
Val	Glu	Ala	Thr	Asn 215	Arg	Leu	Gly	Ser	Ala 220	Arg	Ser	Asp	Val	Leu 225
Thr	Leu	Asp	Ile	Leu 230	Asp	Val	Val	Thr	Thr 235	Asp	Pro	Pro	Pro	Asp 240
Val	His	Val	Ser	Arg 245	Val	Gly	Gly	Leu	Glu 250	Asp	Gln	Leu	Ser	Val 255
Arg	Trp	Val	Ser	Pro 260	Pro	Ala	Leu	Lys	Asp 265	Phe	Leu	Phe	Gln	Ala 270
Lys	Tyr	Gln	Ile	Arg 275	Tyr	Arg	Val	Glu	Asp 280	Ser	Val	Asp	Trp	Lys 285
Val	Val	Asp	Asp	Val 290	Ser	Asn	Gln	Thr	Ser 295	Cys	Arg	Leu	Ala	Gly 300
Leu	Lys	Pro	Gly	Thr 305	Val	Tyr	Phe	Val	Gln 310	Val	Arg	Cys	Asn	Pro 315
Phe	Gly	Ile	Tyr	Gly 320	Ser	Lys	Lys	Ala	Gly 325	Ile	Trp	Ser	Glu	Trp 330
Ser	His	Pro	Thr	Ala 335	Ala	Ser	Thr	Pro	Arg 340	Ser	Glu	Arg	Pro	Gly 345
Pro	Gly	Gly	Gly	Ala	Cys	Glu	Pro	Arg	Gly	Gly	Glu	Pro	Ser	Ser

350	355	360
Gly Pro Val Arg Arg Glu Leu Lys Gln	Phe Leu Gly Trp Leu Lys	
365	370	375
Lys His Ala Tyr Cys Ser Asn Leu Ser	Phe Arg Leu Tyr Asp Gln	
380	385	390
Trp Arg Ala Trp Met Gln Lys Ser His	Lys Thr Arg Asn Gln Asp	
395	400	405
Glu Gly Ile Leu Pro Ser Gly Arg Arg	Gly Thr Ala Arg Gly Pro	
410	415	420

Ala Arg

<210> 33  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 33  
 cccgccccgac gtgcacgtga gcc 23

<210> 34  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 34  
 tgagccagcc caggaactgc ttg 23

<210> 35  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 35  
 caagtgcgct gcaaccctt tggcatctat ggctccaaga aagccgggat 50

<210> 36  
 <211> 1771  
 <212> DNA  
 <213> Homo Sapien

<400> 36  
 cccacgcgtc cgctggtgtt agatcgagca accctctaaa agcagtttag 50

agtggtaaaa	aaaaaaaaaaa	acacaccaaa	cgctcgcagc	cacaaaaggg	100
atgaaatttc	ttctggacat	cctcctgctt	ctcccgttac	tgatcgtctg	150
ctccctagag	tccttcgtga	agctttttat	tcctaagagg	agaaaatcag	200
tcaccggcga	aatcgtgctg	attacaggag	ctgggcacatg	aattgggaga	250
ctgactgcct	atgaatttgc	taaacttaaa	agcaagctgg	ttctctggga	300
tataaataag	catggactgg	aggaaacagc	tgccaaatgc	aagggactgg	350
gtgccaaagg	tcataccttt	gtggtagact	gcagcaaccg	agaagatatt	400
tacagctctg	caaagaagg	gaaggcagaa	attggagatg	ttagtatttt	450
agtaaataat	gctggtgtag	tctatacatc	agatttgttt	gctacacaag	500
atcctcagat	tgaaaagact	tttgaagtta	atgtacttgc	acattttctg	550
actacaaagg	catttcttcc	tgcaatgacg	aagaataacc	atggccatat	600
tgctactgtg	gcttcggcag	ctggacatgt	ctcggtcccc	ttcttactgg	650
cttactgttc	aagcaagttt	gctgctgttg	gatttcataa	aactttgaca	700
gatgaactgg	ctgccttaca	aataactgga	gtcaaaacaa	catgtctgtg	750
tcctaatttc	gtaaacactg	gcttcatcaa	aatccaagt	acaagtttgg	800
gaccactct	ggaacctgag	gaagtggtaa	acaggctgat	gcatgggatt	850
ctgactgagc	agaagatgat	ttttattcca	tcttctatag	cttttttaac	900
aacattggaa	aggatccttc	ctgagcgttt	cctggcagtt	ttaaaacgaa	950
aaatcagtgt	taagtttgat	gcagttattg	gatataaaat	gaaagcgcaa	1000
taagcaccta	gttttctgaa	aactgattta	ccagggttag	gttgatgtca	1050
tctaatagtg	ccagaatttt	aatgtttgaa	cttctgtttt	ttctaattat	1100
ccccatttct	tcaatatcat	ttttgaggct	ttggcagtct	tcatttacta	1150
ccacttgttc	tttagccaaa	agctgattac	atatgatata	aacagagaaa	1200
tacctttaga	ggtgacttta	aggaaaatga	agaaaaagaa	ccaaaatgac	1250
tttattaaaa	taatttccaa	gattatttgt	ggctcacctg	aaggctttgc	1300
aaaatttgta	ccataaccgt	ttatttaaca	tatattttta	tttttgattg	1350
cacttaaatt	ttgtataatt	tgtgtttctt	tttctgttct	acataaaatc	1400
agaaacttca	agctctctaa	ataaaatgaa	ggactatata	tagtgggtatt	1450
tcacaatgaa	tatcatgaac	tctcaatggg	taggtttcat	cctacccatt	1500

Table 1. Demographic characteristics of the study population	
Age (years)	50.0 ± 10.0
Gender	
Male	100 (100%)
Female	0 (0%)
Marital status	
Married	100 (100%)
Single	0 (0%)
Divorced	0 (0%)
Widowed	0 (0%)
Education level	
High school or above	100 (100%)
Below high school	0 (0%)
Occupation	
Managerial	100 (100%)
Professional	0 (0%)
Technical	0 (0%)
Skilled	0 (0%)
Unskilled	0 (0%)
Retired	0 (0%)
Unemployed	0 (0%)
Income (USD/month)	
< 1000	100 (100%)
1000-2000	0 (0%)
> 2000	0 (0%)
Health status	
Good	100 (100%)
Fair	0 (0%)
Poor	0 (0%)
Chronic diseases	
Hypertension	100 (100%)
Diabetes	0 (0%)
Coronary artery disease	0 (0%)
Chronic kidney disease	0 (0%)
Chronic liver disease	0 (0%)
Chronic lung disease	0 (0%)
Chronic mental illness	0 (0%)
Chronic pain	0 (0%)
Chronic disability	0 (0%)
Chronic substance use	0 (0%)
Chronic alcohol use	0 (0%)
Chronic tobacco use	0 (0%)
Chronic drug use	0 (0%)
Chronic medical treatment	0 (0%)
Chronic hospitalization	0 (0%)
Chronic nursing home placement	0 (0%)
Chronic long-term care	0 (0%)
Chronic social isolation	0 (0%)
Chronic loneliness	0 (0%)
Chronic depression	0 (0%)
Chronic anxiety	0 (0%)
Chronic stress	0 (0%)
Chronic fatigue	0 (0%)
Chronic pain	0 (0%)
Chronic disability	0 (0%)
Chronic substance use	0 (0%)
Chronic alcohol use	0 (0%)
Chronic tobacco use	0 (0%)
Chronic drug use	0 (0%)
Chronic medical treatment	0 (0%)
Chronic hospitalization	0 (0%)
Chronic nursing home placement	0 (0%)
Chronic long-term care	0 (0%)
Chronic social isolation	0 (0%)
Chronic loneliness	0 (0%)
Chronic depression	0 (0%)
Chronic anxiety	0 (0%)
Chronic stress	0 (0%)
Chronic fatigue	0 (0%)
Chronic pain	0 (0%)
Chronic disability	0 (0%)
Chronic substance use	0 (0%)
Chronic alcohol use	0 (0%)
Chronic tobacco use	0 (0%)
Chronic drug use	0 (0%)
Chronic medical treatment	0 (0%)
Chronic hospitalization	0 (0%)
Chronic nursing home placement	0 (0%)
Chronic long-term care	0 (0%)
Chronic social isolation	0 (0%)
Chronic loneliness	0 (0%)
Chronic depression	0 (0%)
Chronic anxiety	0 (0%)
Chronic stress	0 (0%)
Chronic fatigue	0 (0%)
Chronic pain	0 (0%)
Chronic disability	0 (0%)
Chronic substance use	0 (0%)
Chronic alcohol use	0 (0%)
Chronic tobacco use	0 (0%)
Chronic drug use	0 (0%)
Chronic medical treatment	0 (0%)
Chronic hospitalization	0 (0%)
Chronic nursing home placement	0 (0%)
Chronic long-term care	0 (0%)
Chronic social isolation	0 (0%)
Chronic loneliness	0 (0%)
Chronic depression	0 (0%)
Chronic anxiety	0 (0%)
Chronic stress	0 (0%)
Chronic fatigue	0 (0%)
Chronic pain	0 (0%)
Chronic disability	0 (0%)
Chronic substance use	0 (0%)
Chronic alcohol use	0 (0%)
Chronic tobacco use	0 (0%)
Chronic drug use	0 (0%)
Chronic medical treatment	0 (0%)
Chronic hospitalization	0 (0%)
Chronic nursing home placement	0 (0%)
Chronic long-term care	0 (0%)
Chronic social isolation	0 (0%)
Chronic loneliness	0 (0%)
Chronic depression	0 (0%)
Chronic anxiety	0 (0%)
Chronic stress	0 (0%)
Chronic fatigue	0 (0%)
Chronic pain	0 (0%)
Chronic disability	0 (0%)
Chronic substance use	0 (0%)
Chronic alcohol use	0 (0%)
Chronic tobacco use	0 (0%)
Chronic drug use	0 (0%)
Chronic medical treatment	0 (0%)
Chronic hospitalization	0 (0%)
Chronic nursing home placement	0 (0%)
Chronic long-term care	0 (0%)
Chronic social isolation	0 (0%)
Chronic loneliness	0 (0%)
Chronic depression	0 (0%)
Chronic anxiety	0 (0%)
Chronic stress	0 (0%)
Chronic fatigue	0 (0%)
Chronic pain	0 (0%)
Chronic disability	0 (0%)
Chronic substance use	0 (0%)
Chronic alcohol use	0 (0%)
Chronic tobacco use	0 (0%)
Chronic drug use	0 (0%)
Chronic medical treatment	0 (0%)
Chronic hospitalization	0 (0%)
Chronic nursing home placement	0 (0%)
Chronic long-term care	0 (0%)
Chronic social isolation	0 (0%)
Chronic loneliness	0 (0%)
Chronic depression	0 (0%)
Chronic anxiety	0 (0%)
Chronic stress	0 (0%)
Chronic fatigue	0 (0%)
Chronic pain	0 (0%)
Chronic disability	0 (0%)
Chronic substance use	0 (0%)
Chronic alcohol use	0 (0%)
Chronic tobacco use	0 (0%)

<211> 300

<213> Homo Sapien

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile  
1 5 10 15

Val Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg  
20 25 30

Arg Lys Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly  
35 40 45

His Gly Ile Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys  
50 55 60

Ser Lys Leu Val Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu  
65 70 75

Thr Ala Ala Lys Cys Lys Gly Leu Gly Ala Lys Val His Thr Phe  
80 85 90

Val Val Asp Cys Ser Asn Arg Glu Asp Ile Tyr Ser Ser Ala Lys  
95 100 105

Lys Val Lys Ala Glu Ile Gly Asp Val Ser Ile Leu Val Asn Asn  
110 115 120

Ala Gly Val Val Tyr Thr Ser Asp Leu Phe Ala Thr Gln Asp Pro  
125 130 135

Gln Ile Glu Lys Thr Phe Glu Val Asn Val Leu Ala His Phe Trp  
140 145 150

Thr Thr Lys Ala Phe Leu Pro Ala Met Thr Lys Asn Asn His Gly  
155 160 165

His Ile Val Thr Val Ala Ser Ala Ala Gly His Val Ser Val Pro  
170 175 180

Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe  
185 190 195

His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile Thr Gly





	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

<210> 42

<211> 243  
 <212> PRT  
 <213> Homo Sapien

<400> 42

Met	Arg	Pro	Leu	Leu	Val	Leu	Leu	Leu	Leu	Gly	Leu	Ala	Ala	Gly	1	5	10	15
Ser	Pro	Pro	Leu	Asp	Asp	Asn	Lys	Ile	Pro	Ser	Leu	Cys	Pro	Gly	20	25	30	
His	Pro	Gly	Leu	Pro	Gly	Thr	Pro	Gly	His	His	Gly	Ser	Gln	Gly	35	40	45	
Leu	Pro	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Ala	Pro	Gly	50	55	60	
Ala	Pro	Gly	Glu	Lys	Gly	Glu	Gly	Gly	Arg	Pro	Gly	Leu	Pro	Gly	65	70	75	
Pro	Arg	Gly	Asp	Pro	Gly	Pro	Arg	Gly	Glu	Ala	Gly	Pro	Ala	Gly	80	85	90	
Pro	Thr	Gly	Pro	Ala	Gly	Glu	Cys	Ser	Val	Pro	Pro	Arg	Ser	Ala	95	100	105	
Phe	Ser	Ala	Lys	Arg	Ser	Glu	Ser	Arg	Val	Pro	Pro	Pro	Ser	Asp	110	115	120	
Ala	Pro	Leu	Pro	Phe	Asp	Arg	Val	Leu	Val	Asn	Glu	Gln	Gly	His	125	130	135	
Tyr	Asp	Ala	Val	Thr	Gly	Lys	Phe	Thr	Cys	Gln	Val	Pro	Gly	Val	140	145	150	
Tyr	Tyr	Phe	Ala	Val	His	Ala	Thr	Val	Tyr	Arg	Ala	Ser	Leu	Gln	155	160	165	
Phe	Asp	Leu	Val	Lys	Asn	Gly	Glu	Ser	Ile	Ala	Ser	Phe	Phe	Gln	170	175	180	
Phe	Phe	Gly	Gly	Trp	Pro	Lys	Pro	Ala	Ser	Leu	Ser	Gly	Gly	Ala	185	190	195	
Met	Val	Arg	Leu	Glu	Pro	Glu	Asp	Gln	Val	Trp	Val	Gln	Val	Gly	200	205	210	
Val	Gly	Asp	Tyr	Ile	Gly	Ile	Tyr	Ala	Ser	Ile	Lys	Thr	Asp	Ser	215	220	225	
Thr	Phe	Ser	Gly	Phe	Leu	Val	Tyr	Ser	Asp	Trp	His	Ser	Ser	Pro	230	235	240	
Val	Phe	Ala																

<210> 43  
 <211> 24

TABLE 1	
Summary of the results of the 1996-1997 survey of the prevalence of <i>Salmonella</i> spp. in the faeces of <i>Salicorina</i> spp. in the coastal zone of the Mediterranean Sea	
Location	Prevalence (%)
Algeria	100
France	100
Italy	100
Spain	100
Tunisia	100
Yugoslavia	100
Other countries	100
Total	100
Number of <i>Salicorina</i> spp. faecal samples analysed	
Algeria	100
France	100
Italy	100
Spain	100
Tunisia	100
Yugoslavia	100
Other countries	100
Total	100
Number of <i>Salmonella</i> spp. isolates	
Algeria	100
France	100
Italy	100
Spain	100
Tunisia	100
Yugoslavia	100
Other countries	100
Total	100
Number of <i>Salmonella</i> spp. isolates identified	
Algeria	100
France	100
Italy	100
Spain	100
Tunisia	100
Yugoslavia	100
Other countries	100
Total	100
Number of <i>Salmonella</i> spp. isolates identified by serotyping	
Algeria	100
France	100
Italy	100
Spain	100
Tunisia	100
Yugoslavia	100
Other countries	100
Total	100
Number of <i>Salmonella</i> spp. isolates identified by phage typing	
Algeria	100
France	100
Italy	100
Spain	100
Tunisia	100
Yugoslavia	100
Other countries	100
Total	100

```
<400> 43
tacaggccca gtcaggacca gggg 24
```

```
<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Synthetic oligonucleotide probe

```
<400> 44
agccagcctc gctctcgg 18
```

```
<210> 45
<211> 18
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Synthetic oligonucleotide probe

```
<400> 45
gtctgcgatc aggtctgg 18
```

```
<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Synthetic oligonucleotide probe

```
<400> 46
gaaagaggca atggattcgc 20
```

```
<210> 47
<211> 24
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Synthetic oligonucleotide probe

```
<400> 47
gacttacact tgccagcaca gcac 24
```

```
<210> 48
<211> 45
<212> DNA
<213> Artificial Sequence
```

[illegible]

```
<400> 48
ggagcaccac caactggagg gtccggagta qcgaqcqccc cqaag 45
```

<211> 1876

<213> Homo Sapien

ctcttttgtc	caccagccca	gcctgactcc	tggagattgt	gaatagctcc	50
atccagcctg	agaaacaagc	cggttggtctg	agccaggtctg	tgcacggagc	100
acctgacggg	cccaacagac	ccatgctgca	tccagagacc	tcccctggcc	150
gggggcatct	cctggctgtg	ctcctggccc	tccttggcac	cacctgggca	200
gaggtgtggc	caccccagct	gcaggagcag	gctccgatgg	ccggagccct	250
gaacaggaag	gagagtttct	tgtctctctc	cctgcacaac	cgcttgcgca	300
gctgggtcca	gccccctgcg	gctgacatgc	ggaggctgga	ctggagtgac	350
agcctggccc	aactggctca	agccagggca	gccctctgtg	gaatcccaac	400
cccgagcctg	gcatccggcc	tgtggcgcac	cctgcaagtg	ggctggaaca	450
tgcagctgct	gcccgcgggc	ttggcgctct	ttgttgaagt	ggtcagccta	500
tggtttgcag	aggggcagcg	gtacagccac	gcggcaggag	agtgtgctcg	550
caacgccacc	tgcacccact	acacgcagct	cgtgtgggcc	acctcaagcc	600
agctgggctg	tgggcggcac	ctgtgctctg	caggccagac	agcgatagaa	650
gcctttgtct	gtgcctactc	ccccggaggc	aactgggagg	tcaacgggaa	700
gacaatcatc	ccctataaga	agggtgccctg	gtgttgcctc	tgcacagcca	750
gtgtctcagg	ctgcttcaaa	gcctgggacc	atgcaggggg	gctctgtgag	800
gtccccagga	atccttgtcg	catgagctgc	cagaaccatg	gacgtctcaa	850
catcagcacc	tgccactgcc	actgtccccc	tggctacacg	ggcagatact	900
gccaagtgag	gtgcagcctg	cagtgtgtgc	acggccgggt	ccgggaggag	950
gagtgtctcg	gcgtctgtga	catcggttac	gggggagccc	agtgtgccac	1000
caaggtgcat	tttcccttcc	acacctgtga	cctgaggatc	gacggagact	1050
gttcatgggt	gtcttcagag	gcagacacct	attacagagc	caggatgaaa	1100
tgtcagagga	aaggcgggggt	gctggcccag	atcaagagcc	agaaagtqca	1150



				110					115					120
Val	Glu	Val	Val	Ser 125	Leu	Trp	Phe	Ala	Glu	Gly	Gln	Arg	Tyr	Ser 135
His	Ala	Ala	Gly	Glu 140	Cys	Ala	Arg	Asn	Ala	Thr	Cys	Thr	His	Tyr 150
Thr	Gln	Leu	Val	Trp 155	Ala	Thr	Ser	Ser	Gln	Leu	Gly	Cys	Gly	Arg 165
His	Leu	Cys	Ser	Ala 170	Gly	Gln	Thr	Ala	Ile	Glu	Ala	Phe	Val	Cys 180
Ala	Tyr	Ser	Pro	Gly 185	Gly	Asn	Trp	Glu	Val	Asn	Gly	Lys	Thr	Ile 195
Ile	Pro	Tyr	Lys	Lys 200	Gly	Ala	Trp	Cys	Ser	Leu	Cys	Thr	Ala	Ser 210
Val	Ser	Gly	Cys	Phe 215	Lys	Ala	Trp	Asp	His	Ala	Gly	Gly	Leu	Cys 225
Glu	Val	Pro	Arg	Asn 230	Pro	Cys	Arg	Met	Ser	Cys	Gln	Asn	His	Gly 240
Arg	Leu	Asn	Ile	Ser 245	Thr	Cys	His	Cys	His	Cys	Pro	Pro	Gly	Tyr 255
Thr	Gly	Arg	Tyr	Cys 260	Gln	Val	Arg	Cys	Ser	Leu	Gln	Cys	Val	His 270
Gly	Arg	Phe	Arg	Glu 275	Glu	Glu	Cys	Ser	Cys	Val	Cys	Asp	Ile	Gly 285
Tyr	Gly	Gly	Ala	Gln 290	Cys	Ala	Thr	Lys	Val	His	Phe	Pro	Phe	His 300
Thr	Cys	Asp	Leu	Arg 305	Ile	Asp	Gly	Asp	Cys	Phe	Met	Val	Ser	Ser 315
Glu	Ala	Asp	Thr	Tyr 320	Tyr	Arg	Ala	Arg	Met	Lys	Cys	Gln	Arg	Lys 330
Gly	Gly	Val	Leu	Ala 335	Gln	Ile	Lys	Ser	Gln	Lys	Val	Gln	Asp	Ile 345
Leu	Ala	Phe	Tyr	Leu 350	Gly	Arg	Leu	Glu	Thr	Thr	Asn	Glu	Val	Thr 360
Asp	Ser	Asp	Phe	Glu 365	Thr	Arg	Asn	Phe	Trp	Ile	Gly	Leu	Thr	Tyr 375
Lys	Thr	Ala	Lys	Asp 380	Ser	Phe	Arg	Trp	Ala	Thr	Gly	Glu	His	Gln 390
Ala	Phe	Thr	Ser	Phe 395	Ala	Phe	Gly	Gln	Pro	Asp	Asn	His	Gly	Leu 405

Val Trp Leu Ser Ala Ala Met Gly Phe Gly Asn Cys Val Glu Leu  
410 415 420

Gln Ala Ser Ala Ala Phe Asn Trp Asn Asp Gln Arg Cys Lys Thr  
425 430 435

Arg Asn Arg Tyr Ile Cys Gln Phe Ala Gln Glu His Ile Ser Arg  
440 445 450

Trp Gly Pro Gly Ser  
455

<210> 51  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 51  
aggaacttct ggatcgggct cacc 24

<210> 52  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 52  
gggtctgggc caggtggaag agag 24

<210> 53  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 53  
gccaaggact ccttccgctg ggccacaggg gagcaccagg ccttc 45

<210> 54  
<211> 2331  
<212> DNA  
<213> Homo Sapien

<400> 54  
cggacgcgtg ggctgggcgc tgcaaagcgt gtcccgccgg gtcccgagc 50  
gtcccgccgc ctgcgccgc catgctcctg ctgctggggc tgtgcctggg 100  
gctgtccctg tgtgtggggc cgcaggaaga ggcgcagagc tggggccact 150  
cttcggagca ggatggactc aggggtcccga ggcaagtcag actgttgcag 200



aggctgaaaa ccaaaccttt gatgacagaa ttctcagtga agtctaccat 250  
catttcccggt tatgccttca ctacgggtttc ctgcagaatg ctgaacagag 300  
cttctgaaga ccaggacatt gagttccaga tgcagattcc agctgcagct 350  
ttcatcacca acttcactat gcttattgga gacaagggtgt atcagggcga 400  
aattacagag agagaaaaga agagtgggtga tagggtaaaa gagaaaagga 450  
ataaaaccac agaagaaaat ggagagaagg ggactgaaat attcagagct 500  
tctgcagtga ttcccagcaa ggacaaagcc gcctttttcc tgagttatga 550  
ggagcttctg cagaggcgcc tgggcaagta cgagcacagc atcagcgtgc 600  
ggccccagca gctgtccggg aggctgagcg tggacgtgaa tatectggag 650  
agcgcgggca tcgcatccct ggagggtgtg ccgcttcaca acagcaggca 700  
gaggggagct gggcgcgggg aagatgattc tgggcctccc ccactactg 750  
tcattaacca aaatgaaaca ttgccaaca taatttttaa acctactgta 800  
gtacaacaag ccaggattgc ccagaatgga attttgggag actttatcat 850  
tagatatgac gtcaatagag aacagagcat tggggacatc caggttctaa 900  
atggctattt tgtgcactac ttgtctcta aagaccttc tcttttacc 950  
aagaatgtgg tattcgtgct tgacagcagt gcttctatgg tgggaaccaa 1000  
actccggcag accaaggatg cctcttcac aattctccat gacctccgac 1050  
cccaggaccg tttcagtatc attggatttt ccaaccggat caaagtatgg 1100  
aaggaccact tgatatcagt cactccagac agcatcaggg atgggaaagt 1150  
gtacattcac catatgtcac ccactggagg cacagacatc aacggggccc 1200  
tgcagagggc catcaggctc ctcaacaagt acgtggccca cagtggcatt 1250  
ggagaccgga gcgtgtccct catcgtcttc ctgacggatg ggaagcccac 1300  
ggtcggggag acgcacaccc tcaagatcct caacaacacc cgagaggccg 1350  
cccagggcca agtctgcac ttcaccattg gcacggcaa cgacgtggac 1400  
ttcaggctgc tggagaaact gtcgtggag aactgtggcc tcacacggcg 1450  
cgtgcacgag gaggaggacg caggctcgca gctcatcggg ttctacgatg 1500  
aaatcaggac cccgtctctc tctgacatcc gcacgatta tccccccagc 1550  
tcagtgggtgc aggccaccaa gacctgttc cccaactact tcaacggctc 1600  
ggagatcatc attgcgggga agctgggtgga caggaagctg gatcacctgc 1650



Arg Val Lys Glu Lys Arg Asn Lys Thr Thr Glu Glu Asn Gly Glu	125	130	135
Lys Gly Thr Glu Ile Phe Arg Ala Ser Ala Val Ile Pro Ser Lys	140	145	150
Asp Lys Ala Ala Phe Phe Leu Ser Tyr Glu Glu Leu Leu Gln Arg	155	160	165
Arg Leu Gly Lys Tyr Glu His Ser Ile Ser Val Arg Pro Gln Gln	170	175	180
Leu Ser Gly Arg Leu Ser Val Asp Val Asn Ile Leu Glu Ser Ala	185	190	195
Gly Ile Ala Ser Leu Glu Val Leu Pro Leu His Asn Ser Arg Gln	200	205	210
Arg Gly Ser Gly Arg Gly Glu Asp Asp Ser Gly Pro Pro Pro Ser	215	220	225
Thr Val Ile Asn Gln Asn Glu Thr Phe Ala Asn Ile Ile Phe Lys	230	235	240
Pro Thr Val Val Gln Gln Ala Arg Ile Ala Gln Asn Gly Ile Leu	245	250	255
Gly Asp Phe Ile Ile Arg Tyr Asp Val Asn Arg Glu Gln Ser Ile	260	265	270
Gly Asp Ile Gln Val Leu Asn Gly Tyr Phe Val His Tyr Phe Ala	275	280	285
Pro Lys Asp Leu Pro Pro Leu Pro Lys Asn Val Val Phe Val Leu	290	295	300
Asp Ser Ser Ala Ser Met Val Gly Thr Lys Leu Arg Gln Thr Lys	305	310	315
Asp Ala Leu Phe Thr Ile Leu His Asp Leu Arg Pro Gln Asp Arg	320	325	330
Phe Ser Ile Ile Gly Phe Ser Asn Arg Ile Lys Val Trp Lys Asp	335	340	345
His Leu Ile Ser Val Thr Pro Asp Ser Ile Arg Asp Gly Lys Val	350	355	360
Tyr Ile His His Met Ser Pro Thr Gly Gly Thr Asp Ile Asn Gly	365	370	375
Ala Leu Gln Arg Ala Ile Arg Leu Leu Asn Lys Tyr Val Ala His	380	385	390
Ser Gly Ile Gly Asp Arg Ser Val Ser Leu Ile Val Phe Leu Thr	395	400	405
Asp Gly Lys Pro Thr Val Gly Glu Thr His Thr Leu Lys Ile Leu			

Asn Asn Thr Arg	Glu Ala Ala Arg Gly Gln Val Cys Ile Phe Thr	410	415	420
	425		430	435
Ile Gly Ile Gly	Asn Asp Val Asp Phe Arg Leu Leu Glu Lys Leu	440	445	450
Ser Leu Glu Asn Cys Gly Leu Thr Arg	Arg Val His Glu Glu Glu	455	460	465
Asp Ala Gly Ser Gln Leu Ile Gly Phe Tyr Asp Glu Ile Arg Thr		470	475	480
Pro Leu Leu Ser Asp Ile Arg Ile Asp Tyr Pro Pro Ser Ser Val		485	490	495
Val Gln Ala Thr Lys Thr Leu Phe Pro Asn Tyr Phe Asn Gly Ser		500	505	510
Glu Ile Ile Ile Ala Gly Lys Leu Val Asp Arg Lys Leu Asp His		515	520	525
Leu His Val Glu Val Thr Ala Ser Asn Ser Lys Lys Phe Ile Ile		530	535	540
Leu Lys Thr Asp Val Pro Val Arg Pro Gln Lys Ala Gly Lys Asp		545	550	555
Val Thr Gly Ser Pro Arg Pro Gly Gly Asp Gly Glu Gly Asp Thr		560	565	570
Asn His Ile Glu Arg Leu Trp Ser Tyr Leu Thr Thr Lys Glu Leu		575	580	585
Leu Ser Ser Trp Leu Gln Ser Asp Asp Glu Pro Glu Lys Glu Arg		590	595	600
Leu Arg Gln Arg Ala Gln Ala Leu Ala Val Ser Tyr Arg Phe Leu		605	610	615
Thr Pro Phe Thr Ser Met Lys Leu Arg Gly Pro Val Pro Arg Met		620	625	630
Asp Gly Leu Glu Glu Ala His Gly Met Ser Ala Ala Met Gly Pro		635	640	645
Glu Pro Val Val Gln Ser Val Arg Gly Ala Gly Thr Gln Pro Gly		650	655	660
Pro Leu Leu Lys Lys Pro Asn Ser Val Lys Lys Lys Gln Asn Lys		665	670	675
Thr Lys Lys Arg His Gly Arg Asp Gly Val Phe Pro Leu His His		680	685	690
Leu Gly Ile Arg				

[illegible]

<400> 56  
gtgggaacca aactccggca gacc 24

<220>  
<223> Synthetic oligonucleotide probe

```
<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Synthetic oligonucleotide probe

```
<400> 58
agccgctcct tctccgggtc atcg 24
```

```
<210> 59
<211> 48
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Synthetic oligonucleotide probe

```
<400> 59
tggaaggacc acttgatata agtcaactcca gacagcatca gggatggg 48
```

```
<210> 60
<211> 1413
<212> DNA
<213> Homo Sapien
```

45

cagttgcaa gtcaataaga gtgacgactc tgtgattcag ctactgaatc 250  
ccaacaggca gaccatttat ttcagggact tcaggccttt gaaggacagc 300  
aggtttcagt tgctgaattt ttctagcagt gaactcaaag tatcattgac 350  
aaacgtctca atttctgatg aaggaagata cttttgccag ctctataaccg 400  
atccccaca ggaaagtac accaccatca cagtcctggg cccaccacgt 450  
aatctgatga tcgatatcca gaaagacact gcggtggaag gtgaggagat 500  
tgaagtcaac tgcactgcta tggccagcaa gccagccacg actatcaggt 550  
ggttcaaagg gaacacagag ctaaaaggca aatcggaggt ggaagagtgg 600  
tcagacatgt aactgtgac cagtcagctg atgctgaagg tgcacaagga 650  
ggacgatggg gtcccagtga tctgccaggt ggagcaccct gcggtcactg 700  
gaaacctgca gaccagcgg tatctagaag tacagtataa gcctcaagtg 750  
cacattcaga tgacttatcc tctacaaggc ttaaccggg aaggggacgc 800  
gcttgagtta acatgtgaag ccacgggaa gccccagcct gtgatggtaa 850  
cttgggtgag agtcgatgat gaaatgcctc aacacgccgt actgtctggg 900  
cccaacctgt tcatcaataa cctaaacaaa acagataatg gtacataaccg 950  
ctgtgaagct tcaaacatag tggggaaagc tcaactcgat tatatgctgt 1000  
atgtatacga tccccccaca actatccctc ctcccacaac aaccaccacc 1050  
accaccacca ccaccaccac caccatcctt accatcatca cagattcccg 1100  
agcaggtgaa gaaggctcga tcagggcagt ggatcatgcc gtgatcggtg 1150  
gcgtcgtggc ggtggtggtg ttgccatgc tgtgcttgct catcattctg 1200  
gggcgtatt ttgccagaca taaaggtaaa tacttcactc atgaagccaa 1250  
aggagccgat gacgcagcag acgcagacac agctataatc aatgcagaag 1300  
gaggacagaa caactccgaa gaaaagaaag agtacttcat ctagatcagc 1350  
ctttttgttt caatgaggtg tccaactggc cctattttaga tgataaagag 1400  
acagtatat tgg 1413

<210> 61  
<211> 440  
<212> PRT  
<213> Homo Sapien

<400> 61  
Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala  
1 5 10 15

Ala Ala Ala Ala Ala	Pro Pro Gly Leu Arg	Leu Leu Leu Leu Leu	
20	25	30	
Phe Ser Ala Ala Ala	Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu		
35	40	45	
Phe Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile			
50	55	60	
Ser Cys Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu			
65	70	75	
Asn Pro Asn Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu			
80	85	90	
Lys Asp Ser Arg Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu			
95	100	105	
Lys Val Ser Leu Thr Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr			
110	115	120	
Phe Cys Gln Leu Tyr Thr Asp Pro Pro Gln Glu Ser Tyr Thr Thr			
125	130	135	
Ile Thr Val Leu Val Pro Pro Arg Asn Leu Met Ile Asp Ile Gln			
140	145	150	
Lys Asp Thr Ala Val Glu Gly Glu Glu Ile Glu Val Asn Cys Thr			
155	160	165	
Ala Met Ala Ser Lys Pro Ala Thr Thr Ile Arg Trp Phe Lys Gly			
170	175	180	
Asn Thr Glu Leu Lys Gly Lys Ser Glu Val Glu Glu Trp Ser Asp			
185	190	195	
Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys Val His Lys Glu			
200	205	210	
Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His Pro Ala Val			
215	220	225	
Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln Tyr Lys			
230	235	240	
Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu Thr			
245	250	255	
Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys			
260	265	270	
Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met			
275	280	285	
Pro Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn			
290	295	300	
Leu Asn Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn			





<400> 64  
atcatcacag attcccgagc 20

<210> 65  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 65  
ttcaatctcc tcaccttcca ccgc 24

<210> 66  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 66  
atagctgtgt ctgcgtctgc tgcg 24

<210> 67  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 67  
cgcggcactg atccccacag gtgatgggca gaatctgttt acgaaagacg 50

<210> 68  
<211> 2555  
<212> DNA  
<213> Homo Sapien

<400> 68  
ggggcggggtg gacgcggact cgaacgcagt tgcttcggga cccaggaccc 50  
cctcgggccc gacccgccag gaaagactga ggccgcgccc tgccccgcc 100  
ggctccctgc gccgcgcgcg cctcccgga cagaagatgt gctccagggt 150  
ccctctgctg ctgccgtgc tctgctact ggccctgggg cctgggggtgc 200  
agggctgccc atccggctgc cagtgcagcc agccacagac agtcttctgc 250  
actgcccgcc aggggaccac ggtgccccga gacgtgccac ccgacacggt 300  
ggggctgtac gtctttgaga acggcatcac catgctcgac gcaagcagct 350  
ttgcgggect gccgggectg cagctcctgg acctgtcaca gaaccagatc 400

gccagcctgc gcctgccccg cctgctgctg ctggacctca gccacaacag 450  
 cctcctggcc ctggagccccg gcctcctgga cactgccaac gtggaggcgc 500  
 tgcggctggc tgggtctgggg ctgcagcagc tggacgaggg gctcttcagc 550  
 cgcttgcgca acctccacga cctggatgtg tccgacaacc agctggagcg 600  
 agtgccacct gtgatccgag gcctccgggg cctgacgcgc ctgcggtgg 650  
 ccggcaacac ccgcattgcc cagctgcggc ccgaggacct ggccggcctg 700  
 gctgccctgc aggagctgga tgtgagcaac ctaagcctgc aggccctgcc 750  
 tggcgacctc tcgggacctc tccccgcct gcggctgctg gcagctgccc 800  
 gcaacccctt caactgcgtg tgccccctga gctggtttgg ccctgggtg 850  
 cgcgagagcc acgtcacact ggccagccct gaggagagcg gctgccactt 900  
 ccgcccag aacgctggcc ggctgctcct ggagcttgac tacgccgact 950  
 ttggctgccc agccaccacc accacagcca cagtgccac cagaggccc 1000  
 gtggtgcggg agcccacagc cttgtcttct agcttggtc ctacctggt 1050  
 tagccccaca gcgcgggcca ctgaggcccc cagcccgccc tccactgccc 1100  
 caccgactgt agggcctgtc cccagcccc aggactgccc accgtccacc 1150  
 tgccccaatg ggggcacatg ccacctgggg acacggcacc acctggcgtg 1200  
 cttgtgcccc gaaggcttca cgggcctgta ctgtgagagc cagatggggc 1250  
 aggggacacg gccagccct acaccagtca cgcgaggcc accacggctc 1300  
 ctgacctgg gcctcgagcc ggtgagcccc acctccctgc gcgtggggct 1350  
 gcagcgctac ctccagggga gctccgtgca gctcaggagc ctccgtctca 1400  
 cctatcgcaa cctatcgggc cctgataagc ggctggtgac gctgcgactg 1450  
 cctgcctcgc tcgctgagta cacggtcacc cagctgcggc ccaacgccac 1500  
 ttactccgtc tgtgtcatgc ctttggggcc cgggcgggtg ccggaggggc 1550  
 aggaggcctg cggggaggcc cataacccc cagccgtcca ctccaaccac 1600  
 gccccagtca cccaggcccc cgagggaac ctgcgcctcc tcattgcgcc 1650  
 cgcctggcc gcggtgctcc tggccgcgt ggctgcggtg ggggcagcct 1700  
 actgtgtgcg gcggggggcg gccatggcag cagcggctca ggacaaagg 1750  
 caggtggggc caggggctgg gccctggaa ctggaggag tgaaggtccc 1800  
 cttggagcca ggcccgaagg caacagagg cggtggagag gccctgccc 1850



				110					115					120
Ala	Leu	Arg	Leu	Ala	Gly	Leu	Gly	Leu	Gln	Gln	Leu	Asp	Glu	Gly
				125					130					135
Leu	Phe	Ser	Arg	Leu	Arg	Asn	Leu	His	Asp	Leu	Asp	Val	Ser	Asp
				140					145					150
Asn	Gln	Leu	Glu	Arg	Val	Pro	Pro	Val	Ile	Arg	Gly	Leu	Arg	Gly
				155					160					165
Leu	Thr	Arg	Leu	Arg	Leu	Ala	Gly	Asn	Thr	Arg	Ile	Ala	Gln	Leu
				170					175					180
Arg	Pro	Glu	Asp	Leu	Ala	Gly	Leu	Ala	Ala	Leu	Gln	Glu	Leu	Asp
				185					190					195
Val	Ser	Asn	Leu	Ser	Leu	Gln	Ala	Leu	Pro	Gly	Asp	Leu	Ser	Gly
				200					205					210
Leu	Phe	Pro	Arg	Leu	Arg	Leu	Leu	Ala	Ala	Ala	Arg	Asn	Pro	Phe
				215					220					225
Asn	Cys	Val	Cys	Pro	Leu	Ser	Trp	Phe	Gly	Pro	Trp	Val	Arg	Glu
				230					235					240
Ser	His	Val	Thr	Leu	Ala	Ser	Pro	Glu	Glu	Thr	Arg	Cys	His	Phe
				245					250					255
Pro	Pro	Lys	Asn	Ala	Gly	Arg	Leu	Leu	Leu	Glu	Leu	Asp	Tyr	Ala
				260					265					270
Asp	Phe	Gly	Cys	Pro	Ala	Thr	Thr	Thr	Thr	Ala	Thr	Val	Pro	Thr
				275					280					285
Thr	Arg	Pro	Val	Val	Arg	Glu	Pro	Thr	Ala	Leu	Ser	Ser	Ser	Leu
				290					295					300
Ala	Pro	Thr	Trp	Leu	Ser	Pro	Thr	Ala	Pro	Ala	Thr	Glu	Ala	Pro
				305					310					315
Ser	Pro	Pro	Ser	Thr	Ala	Pro	Pro	Thr	Val	Gly	Pro	Val	Pro	Gln
				320					325					330
Pro	Gln	Asp	Cys	Pro	Pro	Ser	Thr	Cys	Leu	Asn	Gly	Gly	Thr	Cys
				335					340					345
His	Leu	Gly	Thr	Arg	His	His	Leu	Ala	Cys	Leu	Cys	Pro	Glu	Gly
				350					355					360
Phe	Thr	Gly	Leu	Tyr	Cys	Glu	Ser	Gln	Met	Gly	Gln	Gly	Thr	Arg
				365					370					375
Pro	Ser	Pro	Thr	Pro	Val	Thr	Pro	Arg	Pro	Pro	Arg	Ser	Leu	Thr
				380					385					390
Leu	Gly	Ile	Glu	Pro	Val	Ser	Pro	Thr	Ser	Leu	Arg	Val	Gly	Leu
				395					400					405

Gln Arg Tyr Leu Gln Gly Ser Ser Val	Gln Leu Arg Ser Leu Arg
410	415 420
Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr	
425	430 435
Leu Arg Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu	
440	445 450
Arg Pro Asn Ala Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro	
455	460 465
Gly Arg Val Pro Glu Gly Glu Glu Ala Cys Gly Glu Ala His Thr	
470	475 480
Pro Pro Ala Val His Ser Asn His Ala Pro Val Thr Gln Ala Arg	
485	490 495
Glu Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala Leu Ala Ala Val	
500	505 510
Leu Leu Ala Ala Leu Ala Ala Val Gly Ala Ala Tyr Cys Val Arg	
515	520 525
Arg Gly Arg Ala Met Ala Ala Ala Ala Gln Asp Lys Gly Gln Val	
530	535 540
Gly Pro Gly Ala Gly Pro Leu Glu Leu Glu Gly Val Lys Val Pro	
545	550 555
Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly Gly Gly Glu Ala Leu	
560	565 570
Pro Ser Gly Ser Glu Cys Glu Val Pro Leu Met Gly Phe Pro Gly	
575	580 585
Pro Gly Leu Gln Ser Pro Leu His Ala Lys Pro Tyr Ile	
590	595

<210> 70

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

ccctccactg cccaccgac tg 22

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

```

<400> 71
  cggttctggg gacgttaggg ctcg 24

<210> 72
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 72
  ctgcccaccg tccacctgcc tcaat 25

<210> 73
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 73
  aggactgccc accgtccacc tgcctcaatg ggggcacatg ccacc 45

<210> 74
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 74
  acgcaaagcc ctacatctaa gccagagaga gacagggcag ctggg 45

<210> 75
<211> 1077
<212> DNA
<213> Homo Sapien

<400> 75
  ggcactagga caaccttctt cctttctgca ccaactgcccg taccettacc 50
  cgccccgccca cctccttgct accccactct tgaaaccaca gctgttgcca 100
  ggggtccccag ctcatgccag cctcatctcc tttcttgcta gccccaaaag 150
  ggcctccagg caacatgggg ggcccagtca gagagccggc actctcagtt 200
  gccctctggt tgagttgggg ggcagctctg ggggcccgtg cttgtgccat 250
  ggctctgctg acccaacaaa cagagctgca gagcctcagg agagaggtga 300
  gccggctgca ggggacagga ggcccctccc agaatgggga agggatatccc 350
  tggcagagtc tcccggagca gagttccgat gccctggaag cctgggagaa 400

```







caggetcagc agggggccagg ggccacactg gacccaaagg gcagaagggc 700  
 tccatggggg cccctgggga gcggtgcaag agccactacg ccgccttttc 750  
 ggtggggccg aagaagccca tgcacagcaa ccactactac cagacggtga 800  
 tcttcgacac ggagttcgtg aacctctacg accacttcaa catgttcacc 850  
 ggcaagttct actgctacgt gcccggcctc tactttctca gcctcaacgt 900  
 gcacacctgg aaccagaagg agacctacct gcacatcatg aagaacgagg 950  
 aggaggtggt gatcttggtc ggcaggtgg ggcaccgcag catcatgcaa 1000  
 agccagagcc tgatgctgga gctgagagag caggaccagg tgtgggtacg 1050  
 cctctacaag ggcgaacgtg agaacgccat cttcagcgag gagctggaca 1100  
 cctacatcac cttcagtggt tacctggtca agcacgccac cgagccctag 1150  
 ctggccggcc acctccttc ctctcgccac cttccacccc tgcgctgtgc 1200  
 tgacccacc gcctcttccc cgatccctgg actccgactc cctggctttg 1250  
 gcattcagtg agacgccttg cacacacaga aagccaaagg gatcggtgct 1300  
 cccagatccc gcagcctctg gagagagctg acggcagatg aaatcaccag 1350  
 ggcggggcac ccgcgagaac cctctgggac cttccgcggc cctctctgca 1400  
 cacatcctca agtgaccccc cacggcgaga cgcgggtggc ggcagggcgt 1450  
 cccaggggtgc ggcaccgcgg ctccagtcct tggaaataat taggcaaatt 1500  
 ctaaagggtc caaaaggagc aaagtaaacc gtggaggaca aagaaaagg 1550  
 ttgttatttt tgtctttcca gccagcctgc tggctcccaa gagagaggcc 1600  
 ttttcagttg agactctgct taagagaaga tccaaagtta aagctctggg 1650  
 gtcaggggag gggccggggg caggaaacta cctctggctt aattctttta 1700  
 agccacgtag gaactttctt gagggatagg tggaccctga catccctgtg 1750  
 gccttgccca agggctctgc tggcttttct gagtcacagc tgcgaggtga 1800  
 tgggggctgg ggccccaggc gtcagcctcc cagagggaca gctgagcccc 1850  
 ctgccttggc tccaggttgg tagaagcagc cgaagggctc ctgacagtgg 1900  
 ccagggaccc ctgggtcccc caggcctgca gatgtttcta tgaggggcag 1950  
 agtccttgg tacatccatg tgtggctctg ctccaccct gtgccacccc 2000  
 agagccctgg ggggtggtct coatgctgc caccctggca tcggctttct 2050  
 gtgccgcctc ccacacaaat cagccccaga agggcccggg gccttggctt 2100



110	115	120
Ala Arg Gly His Thr Gly Pro Lys Gly Gln Lys Gly Ser Met Gly		
125	130	135
Ala Pro Gly Glu Arg Cys Lys Ser His Tyr Ala Ala Phe Ser Val		
140	145	150
Gly Arg Lys Lys Pro Met His Ser Asn His Tyr Tyr Gln Thr Val		
155	160	165
Ile Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp His Phe Asn Met		
170	175	180
Phe Thr Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu Tyr Phe Phe		
185	190	195
Ser Leu Asn Val His Thr Trp Asn Gln Lys Glu Thr Tyr Leu His		
200	205	210
Ile Met Lys Asn Glu Glu Glu Val Val Ile Leu Phe Ala Gln Val		
215	220	225
Gly Asp Arg Ser Ile Met Gln Ser Gln Ser Leu Met Leu Glu Leu		
230	235	240
Arg Glu Gln Asp Gln Val Trp Val Arg Leu Tyr Lys Gly Glu Arg		
245	250	255
Glu Asn Ala Ile Phe Ser Glu Glu Leu Asp Thr Tyr Ile Thr Phe		
260	265	270
Ser Gly Tyr Leu Val Lys His Ala Thr Glu Pro		
275	280	

<210> 79  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 79  
 tacaggccca gtcaggacca gggg 24

<210> 80  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 80  
 ctgaagaagt agaggccggg cacg 24

<210> 81

[illegible]

```
<400> 81
  cccggtgctt gcgctgctgt gaccccggtg cctccatgta cccgg 45
```

```

<400> 82
gcgagcgcgc cgcgcgcgcgc cgcgcgcgcgc cgcgcgcgcgc gattcgcgcgc 50
tctctctctc ggcgcgcgcgc gagctgtctc cgcacctgga tggcagcagc 100
ggcgcgcgcgc tctctctcgc gccagagaga aatctcatca tctgtgcagc 150
cttctttaaag caaactaaga ccagagggag gattatcctt gacctttgaa 200
gacaaaaact aaactgaaat ttaaaatggt cttcggggga gaaggagct 250
tgacttacac tttggttaata atttgcttcc tgacactaag gctgtctgct 300
agtcagaatt gcctcaaaaa gagtctagaa gatgttgtca ttgacatcca 350
gtcatctctt tctaagggaa tcagaggcaa tgagcccgta tatacttcaa 400
ctcaagaaga ctgcattaat tcttgctggt caacaaaaaa catatcaggg 450
gacaaagcat gtaacttgat gatctctcgc actcgaaaaa cagctagaca 500
acccaactgc tacctatctt tctgtcccaa cgaggaagcc tgtccattga 550
aaccagcaaa aggacttatg agttacagga taattacaga ttttccatct 600
ttgaccagaa atttgccaag ccaagagtta cccaggaag attctctctt 650
acatggccaa ttttcacaag cagtcactcc cctagcccat catcacacag 700
attattcaaa gccacccgat atctcatgga gagacacact ttctcagaag 750
tttggtatct cagatcacct ggagaaacta ttttaagatgg atgaagcaag 800
tgcccagctc cttgcttata aggaaaaagg ccattctcag agttcacaat 850
tttctctgta tcaagaaata gctcatctgc tgctgaaaa tgtgagtgcg 900
ctcccagcta cgggtggcagt tgettctcca cataccacct cggctactcc 950
aaagcccgcg acccttctac ccaccaatgc ttcagtgaca ccttctggga 1000
cttcccagcc acagctggcc accacagctc cactgtaac cactgtcact 1050

```

tctcagcctc ccaagaccct catttctaca gttttttacac gggctgcggc 1100  
 tacactccaa gcaatggcta caacagcagt tetgactacc acctttcagg 1150  
 cacctacgga ctcgaaaggc agcttagaaa ccataccgtt tacagaaatc 1200  
 tccaacttaa ctttgaacac agggaaatgtg tataacccta ctgcactttc 1250  
 tatgtcaa at gtggagtctt ccactatgaa taaaactgct tcctgggaag 1300  
 gtagggaggc cagtcaggc agttcctccc agggcagtg tccagaaaat 1350  
 cagtacggcc ttccatttga aaaatggctt cttatcgggt cctgctctt 1400  
 tgggtgctctg ttctgggtga taggcctcgt cctcctgggt agaatecttt 1450  
 cggaatcact ccgcaggaaa cgttactcaa gactggatta tttgatcaat 1500  
 gggatctatg tggacatcta aggatggaac tcgggtgtctc ttaattcatt 1550  
 tagtaaccag aagcccaaat gcaatgagtt tetgctgact tgctagtctt 1600  
 agcaggaggt tgtattttga agacaggaaa atgccccctt ctgctttcct 1650  
 tttttttttt ggagacagag tcttgcctctg ttgcccaggc tggagtgcag 1700  
 tagcacgac tcggctctca ccgcaacctc cgtctcctgg gttcaagcga 1750  
 ttctcctgcc tcagcctcct aagtatctgg gattacaggc atgtgccacc 1800  
 acacctgggt gattttttgta ttttttagtag agacgggggt tcaccatgtt 1850  
 ggtcaggctg gtctcaaact cctgacctag tgatccaccc tccteggcct 1900  
 cccaaagtgc tgggattaca ggcattgagc accacagctg gcccccttct 1950  
 gtttttatgtt tgggtttttga gaaggaatga agtgggaacc aaattaggta 2000  
 attttgggta atctgtctct aaaatattag ctaaaaacaa agctctatgt 2050  
 aaagtaataa agtataattg ccatataaat ttcaaaattc aactggcttt 2100  
 tatgcaaaga aacagggttag gacatctagg ttccaattca ttcacattct 2150  
 tggttccaga taaaatcaac tgtttatata aatttcta at ggatttgctt 2200  
 ttctttttat atggattcct ttaaaactta ttccagatgt agttccttcc 2250  
 aattaaatat ttgaataaat cttttgttac tcaa 2284

<210> 83  
 <211> 431  
 <212> PRT  
 <213> Homo Sapien

<400> 83  
 Met Phe Phe Gly Gly Glu Gly Ser Leu Thr Tyr Thr Leu Val Ile  
 1 5 10 15





<210> 87  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 87  
 caccgtagct gggagcgcac tcac 24

<210> 88  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 88  
 agtgtaagtc aagctccc 18

<210> 89  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 89  
 gcttcctgac actaaggctg tctgctagtc agaattgcct caaaaagag 49

<210> 90  
 <211> 957  
 <212> DNA  
 <213> Homo Sapien

<400> 90  
 cctggaagat ggcgccattg gctgggtggc tgctcaaggt ggtgttcgtg 50  
 gtcttcgct ccttggtgac ctggtattcg ggtacctgc tcgagagct 100  
 cattccagat gcacccctgt ccagtgtgc ctatagcatc cgcagcatcg 150  
 gggagaggcc tgtcctcaaa gctccagtcc ccaaaaggca aaaatgtgac 200  
 cactggactc cctgcccatac tgacacctat gcctacaggt tactcagcgg 250  
 aggtggcaga agcaagtacg ccaaaatctg ctttgaggat aacctactta 300  
 tgggagaaca gctgggaaat gttgccagag gaataaacat tgccattgtc 350  
 aactatgtaa ctgggaatgt gacagcaaca cgatgttttg atatgtatga 400  
 aggcgataac tctggaccga tgacaaagtt tattcagagt gctgctccaa 450  
 aatccctgct cttcatggtg acctatgacg acggaagcac aagactgaat 500





Asp	Ala	Lys	Asn	Ala	Ile	Glu	Ala	Leu	Gly	Ser	Lys	Glu	Ile	Arg
			170						175					180
Asn	Met	Lys	Phe	Arg	Ser	Ser	Trp	Val	Phe	Ile	Ala	Ala	Lys	Gly
			185						190					195
Leu	Glu	Leu	Pro	Ser	Glu	Ile	Gln	Arg	Glu	Lys	Ile	Asn	His	Ser
			200						205					210
Asp	Ala	Lys	Asn	Asn	Arg	Tyr	Ser	Gly	Trp	Pro	Ala	Glu	Ile	Gln
			215						220					225
Ile	Glu	Gly	Cys	Ile	Pro	Lys	Glu	Arg	Ser					
			230						235					

<210> 92  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 92  
 aatgtgacca ctggactccc 20

<210> 93  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 93  
 aggcttgga ctccttc 18

<210> 94  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 94  
 aagattcttg agcgattcca gctg 24

<210> 95  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 95  
 aatccctgct cttcatgggtg acctatgacg acggaagcac aagactg 47

<210> 96  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 96  
ctcaagaagc acgcgtactg c 21

<210> 97  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 97  
ccaacctcag cttccgcctc tacga 25

<210> 98  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 98  
catccaggct cgccactg 18

<210> 99  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 99  
tggcaaggaa tgggaacagt 20

<210> 100  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 100  
atgctgccag acctgatcgc agaca 25

<210> 101  
<211> 19  
<212> DNA



[illegible]

tggcccagct gacgaqccct 20

<211> 21

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

ctcataggca ctcggttctg q 21

<211> 19

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

tggctcccag cttggaaga 19

<211> 30

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

cagctcttgg ctgtctccag tatgtaccca 30

<211> 21

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

gatgcctctg ttctctgcaca t 21

<211> 48

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

69



